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AL645910 Mouse DNA
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AC149190 Papio anu
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AC16494 Bos tauru
AL591826 BAC 13C18
AC156237 Bas tauru
D00056 Monkey B-1y
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AC161787 Cercopith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 260; DB 6; Length 9: Best Local Similarity 100.0%; Pred. No. 1.7e-67; Matches 260; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 linear
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IVEECASFIPLEAMVAAIDKLKSTITTTSPFTLETALEKLNTFLGPHAATILAIIEYC
CGLVTLPDNPPASCVPAFIAGITTPLPHKIKMFLSLFGGAIASKLTDARGALAFWAG
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1 (bases 1 to 939)

Martin, A., Bodola, F., Sangar, D.V., Goettge, K., Popov, V.,

Rijnbrand, R., Lanford, R.B. and Lemon, S.M.

Chronic hepatitis associated with GB virus B persistence in a tamarin after intrahepatic inoculation of synthetic viral RNA Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9962-9967 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (25-FEB-2003) Virology and Immunology, University of Texas Medical Branch, 301 University Boulevard, Galveston, TX
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Martin,A., Bodola,F., Sangar,D.V., Goettge,K., Popov,V.,
Rijnbrand,R., Lanford,R.E. and Lemon,S.M.
Direct Submission
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Direct Submission

Submitted (23-AUG-1999) Hepatitis Viruses Section, Laboratory of

Infectious Diseases, National Institute of Allergy and Infectious

Diseases, National Institutes of Health, Building 7, Room 201, 7

Center Dr. 0740, Bethesda, MD 20892, USA

Location/Qualifiers

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Toward a surrogate model for hepatitis C virus: An infectious molecular clone of the GB virus-B hepatitis agent Virology 262 (2), 470-478 (1999)
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WSPDAVGATCDTVCFDSTI TPEDIMVETDI YSAAKLSDQHRAGIHTI ARQLYAGGPMI
AYDGREI GYRRCRSSGVYTTSSSNSLTCWLKVNAAAEQAGMKNPRFLI CGDDCTVI WK
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TVYTDWYGRYTVPVBELDESIIAGVHGIEAFSVYRYINAEILRVSQSLTDWTWPPLRA
TRKKARAVLASAKRGGAHAKLARFILWHATSRPLPDLDKTSVARYTTFNYCDVYSPE
GDVFITPQRRLGKFLVKYLAVIVPALGLIAVGLAIS"
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THPIVGPLVAGAVVRRVCQIVRLLEDGVNNATGHRGYHLFVVCLLSLAACPCSGARVT
DPDTNTTILTNCCQRNQVI VSCLELEBGGVI CABEGWVPANPYISHPSNWTGTDS
FLADHI DFVMGALLYCDALDIGELCGACVLVGPWLVRHWLIH DLNETGTCYLEVPG
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QLLLALMLYI EATSGNPI RVPTGCSI AEFCSPLMI PCPCHSYLSENVSEVI CYSPKWT
RPI TLEYNNSI SWY PYTI PGARGCMVKFKNNTWGCCRI RNVPSYCTMGTDAVWNDTRN
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                                                                                                                                                                                                       /noTe="most closely related to hepatitis C virus; experimental infection of tamarins causes acute resolving
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organism="Hepatitis GB virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product="polyprotein"
'protein_id="AAF01368.1"
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                                                 /mol_type="genomic RNA"
/specific_host="unknown"
                                                                                                                                                     db xref="taxon:39113"
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Istituto di Ricerche di Biologia Molecolare P. Angeletti S.p.A.;
Pomezia;
CTGTGCAGAGCGTAGTACCAAGGCTGCACCCCGGTTTTTGTTCCAAGCGGAGGGAACC
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Sequence 1 from patent US 6627437.
AR403987.1 GI:40151915
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Sequence 1 from Patent WO0073466.
AX055777.1 GI:12228889
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/organism="unknown"
/mol_type="genomic DNA"
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                                                                          9380 CCCCCTTGGAATTAAAACT 9399
                                                  CCCGCTTGGAATTAAAACT 260
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1 (bases 1 to 309)
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                                          Gaps
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tch 100.0%; Score 260; DB 13; al Similarity 100.0%; Pred. No. 1.7e-67; 260; Conservative 0; Mismatches 0;
   Query Match
Best Local Similarity
Matches 260; Conserv
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Length 9399;

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De Tomassi, A., Pizzuti, M., Graziani, R., Sbardellati, A.,
Altamura, S., Paonessa, G. and Traboni, C.
Cell clones selected from the Huh7 human hepatoma cell line support
efficient replication of a subgenomic GB virus B replicon
J. Virol. 76 (15), 7736-7746 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (22-JAN-2002) Traboni C., Biochemistry, IRBM P.Angeletti,
via Pontina, Km.30, 600. 00040 Pomezia (Roma), ITALY
related sequence AJ277947.
Location/Qualifiers
join(1...1281,1893...8027)
/organism="Hepatitis GB virus B"
/mol type="RDA"
/isoTate="FL3"
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Hepatitis GB virus B subgenomic replicon neoRepB.
AJ428955
AJ428955.
Gore-neo fusion protein; core-neo gene; polyprotein.
Hepatitis GB virus B
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae.
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/function="core-neo fusion protein"
                                                                   /evidence=experimental
99. .357
/note="3' Y region"
/evidence=experimental
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    .357
    evidence=experimental

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                                     31. .48
/note="poly-U"
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Best Local Similarity 99.6%;
Matches 259; Conservative 0
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Hepatitis GB virus B
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 GAGTTTGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGAT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACGTCCCTTCTGGCTCATCCACAAAACCGTCTCGGGTGAGGAGTCCTGGCTGTG 120
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'note="cDNA complementary to the last 49 published 3'UTR nucleotides of GBV-B plus a novel nucleotide (C) in position 44 and 259 novel nucleotide sequence at the 3'end."
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                                 Traboni,C.I.
Novel gbv sequence
Novel gbv sequence
Patent: WO 0073466-A 1 07-DEC-2000;
ISTITUTO DI RICERCHE DI BIOLOGIA MOLECOLARE P. ANGELETTI; S.P.A.
(IT)
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Ricerche di Biologia Molecolare, Via Pontina. Km. 30.600, 00040
Pomezia, Rome, ITALY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACGTCCCTTCTGGCTCATCCACAAAAACCGTCTCGGGTGAGGGTGAGGAGTCCTGGCTGTG
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Hepatitis GB virus B partial 3'UTR region.
Y18973 Y18973.1 GI:6018427
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                                                                                                                                                                                                                                                                                                                                                              99.4%; Score 258.4; DB 99.6%; Pred. No. 8e-67; cive 0; Mismatches
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J. Virol. 73 (12), 10546-10550 (1999)
                                                                                                                                                                               /mol_type="unassigned DNA"
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                                                                                                                                               1. .309
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                                                                                                                             Location/Qualifiers
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 unclassified sequences
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Traboni, C.
Direct Submission
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Best Local Similarity 99.6
Matches 259; Conservative
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VRL 15-APR-2005

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7930 TGGGAAGCAGTATAAATTCCCGTCGTGTGTGGTGACGCCCTCACGACGTACTTGTCCG 7989
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                                                                                                                                                                                                                                                                                                                                                     7948 CTGTGCAGAGCGTAGTACCAAGGCTGCACCCCGGTTTTTGTTCCAAGCGGAGGGCAACC 8007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     de Tomassi,A., Graziani,R., Paonessa,G. and Traboni,C. GB virus B based replicons and replicon enhanced cells Patent: WO 03059944-A 1 24-JUL-2003; ISTITUTO DI RICERCHE DI BIOLOGIA MOLECOLARE P. ANGELETTI S.P.A. (IT)
                                                                                                                                      7828 GACGICCCIICIGGCICAFCCACAAAACCGICTCGGGIGGGIGAGAGAGACCTGTG
                              7768 GAGITIGGCGACCAIGGIGGAICAGAACCGITICGGGIGAAGCCAIGGICTGAAGGGGAI
                                                                                                                                                                                                                                                                      7888 TGGGAAGCAGTCAGTATAATTCCCGTCGTGTGTGTGGTGACGCCTCACGACGTACTTGTCCG
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                                                                                                          TGGGAAGCAGTCAGTATAATTCCCGTCGTGTGGTGACGCCTCACGACGTATTTGTCCG
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1 GAGITIGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGAT
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Pred. No. 5.2e-67;
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forganism="synthetic construct"
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fnoTe="GBV-B Replicon"
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other sequences; artificial sequences.
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99.4%; Score 258.4;
Best Local Similarity 99.6%; Pred. No. 5.2e
Matches 259; Conservative 0; Mismatches
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Sequence 1 from Patent WO03059944.
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CRSGGYYTTSSSNSLTCWLKVNAAAEQAGMKNPRFLICGDDCTVIWKSAGADADKQAM
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                                                                                                                                        de Tomassi,A., Graziani,R., Paonessa,G. and Traboni,C. GB virus B based replicons and replicon enhanced cells Patent: WO 03059944-A 2 24-JUL-2003; ISTITUTO DI RICERCHE DI BIOLOGIA MOLECOLARE P. ANGELETTI S.P.A. (IT)
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Direct Submission

Birect Submission

Submitted (15-MAY-2000) Traboni C., Biochemistry, IRBM P.

Submitted (15-MAY-2000) Traboni C., Biochemistry, IRBM P.

Angeletti, via Pontina km., 30.600, 00040 Pomezia (Roma), ITALY

Location/Qualifiers

1. 9397

/organism="Hepatitis GB virus B"

/mol_type="genomic RNA"

/db_xref="taxon:39113"
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99.4%; Score 258.4; DB 6; Length 9397;
Best Local Similarity 99.6%; Pred. No. 5.1e-67;
Matches 259; Conservative 0; Mismatches 1; Indels 0;
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J. Gen. Virol. 82 (PT 10), 2437-2448 (2001)
11562537
(bases 1 to 9397)
                                                                                                                                                                                                                                                         Location/Qualifiers
1. .9397
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                                                                                                                      other sequences; artificial sequences.
Sequence 2 from Patent WO03059944.
AX805212
AX805212.1 GI:38522352
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Hepatitis GB virus B
Hepatitis GB virus B
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synthetic construct
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RGKDSTQSAPAKRPTKKKLGKSEFSCSMSYTWTDVISFKTASKVLSATRAITSGFLKQ
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WRKKRAVIASAKRRGGAHAKLARFLLWHATSRPLPDLDKTSVARYTTFNYCDVYSPE
GDVEVTPQRRLQKFLVKYLAVIVFALGLIAVGLAIS"
9041. 9337
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DPDTNTTILTNCCQRNQVIYCSPSTCLHEPGCVICADECWVPANPYISHPSNWTGTDS
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TYEACGVTPWLTTAWHNGSALKLAILQY PGSKEMFKPHNWMSGHLY FEGSDTPIVY FY
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GBV sequence
Patent: US 6627437-A 4 30-SEP-2003;
Istituto di Ricerche di Biologia Molecolare P. Angeletti S.p.A.;
Pomezia;
WOX;
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Batent: US 6627437-A 3 30-SEP-2003;
Istituto di Ricerche di Biologia Molecolare P. Angeletti S.p.A.;
Pomezia;
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Sequence 4 from patent US 6627437.
AR403990. GI:40151918
                                             AR403989 259 bp
Sequence 3 from patent US 6627437.
AR403989
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Unclassified.
1 (bases 1 to 259)
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1 (bases 1 to 259)
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Istituto di Ricerche di Biologia Molecolare P. Angeletti S.p.A.;
Pomezia;
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Pred. No. 5.1e-67;
0; Mismatches 1; Indels 0;
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99.0%; Score 257.4; DB 6; Length 259;
Best Local Similarity 99.6%; Pred. No. 1.6e-66;
Matches 258; Conservative 0; Mismatches 1; Indels 0
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AR403988.1 GI:40151916
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                          Query Match
Best Local Similarity 99.6%;
Matches 259; Conservative
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1 (bases 1 to 259)
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PAT 13-JAN-2001

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181 TGTGCAGAGCGTAGTACCAAGGCTGCACCCCGGTTTTTGTTCCAAGCGGAGGGCAACCC 240
                                                                                                                           Traboni,C.I.
Novel gbv sequence
Novel gbv sequence
Patent: WO 0073466-A 2 07-DEC-2000;
ISTITUTO DI RICERCHE DI BIOLOGIA MOLECOLARE P. ANGELETTI; S.P.A.
(IT)
                                                                                                                                                                                                                                                                                                                                                                1 AGTTTGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGATG
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                                                                                                                                                                                                            1. .259
/organism="unidentified"
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/db xref="taxon:3264"
/noTe="GBV-B-like virus"
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                      259 bp
Sequence 2 from Patent WO0073466.
AX055778
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                                                             AX055778.1 GI:12228890
                                                                                     unidentified
unidentified
unclassified sequences.
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Matches 258; Conservative
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Patent: US 6627437-A 5 30-SEP-2003;
Istituto di Ricerche di Biologia Molecolare P. Angeletti S.p.A.;
Pomazia;
                                                                                                  2 AGTITGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCCATGGTCTGAAGGGGATG
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Score 257.4; DB 6;
Pred. No. 1.6e-66;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                               Sequence 5 from patent US 6627437.
AR403991.1 GI:40151919
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1. .259
/organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                CCGCTTGGAATTAAAACT 260
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Query Match
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Traboni, C.
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Best Local Similarity 99.61
Matches 258; Conservative
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n 5.1.6 Compugen Ltd. , Search time 366 Seconds (without alignments) 4734.481 Million cell updates/sec	.cccgcttggaattaaaaact 260 e8 rs: 9993994			cted by chance to have a sof the result being printed, score distribution.	Aaf23484 GBV-B vir Adj56724 GB virus Ad562010 GBV-B 3'X Ad37751 Hepaitis Ad37751 Hepaitis Ad37752 Genomic h Aac31998 GBV-B 3'X Adj56731 3' termin Adj56731 3' termin Adj6424 GB virus Aac1996 GBV-B 3'X Adj64259 GB virus Adj64254 Hepaitis Adj64254 Hepaitis Adj64254 Hepaitis Adj64254 Hepaitis Adj64254 Hepaitis Adj64254 Hepaitis Adj64254 Hepaitis Adf82149 Leukaemia Aad09560 Human tra Abn25772 Human ORF
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Co OM nucleic - nucleic Run on: Decer	t score: 26 ce: 1 g table: II ed: 49	Minimum DB seq length: Maximum DB seq length: Post-processing: Minimu	Database: N_C 1:-2: 2: 2: 3: 3: 4: 4: 4: 4: 4: 4: 4: 4: 4: 4: 4: 4: 4:	Pred. No. is the score greater the and is derived b secult Query No. Score Match	1 260 100.0 3 260 100.0 4 258.4 99.4 5 258.4 99.4 7 257.4 99.4 8 254.4 99.4 10 248.8 95.7 11 248.4 97.8 12 128.4 94.4 11 248.4 94.4 11 248.4 94.4 12 12 12 12 12 12 12 12 12 12 12 12 12 1

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                                                   9140 GAGTTTGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGAT 9199
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                                                                                                                                  CTGTGCAGAGCGTAGTACCAAGGGCTGCACCCCGGTTTTTGTTCCAAGCGGAGGGCAACC 240
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                                                                                1 GAGTTTGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGAT
                                                                        GACGTCCCTTCTGGCTCATCCACAAAACCGTCTCGGGTGGGGTGAGGAGTCCTGGCTGTG
                                                                                                                                                                                                                                                                           вв; GB virus B; GBV-B; HCV; flavivirus; hepatitis C virus; antiviral; vaccine; virucidal; antinflammatory.
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Seguence 9399 BP; 2125 A; 2326 C; 2430 G; 2518 T; 0 U; 0 Other;
             Query Match 100.0%; Score 260; DB 4; Length 9399; Best Local Similarity 100.0%; Pred. No. 1e-77; Matches 260; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                               /*tag= j
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bound moiety= "GBV-B DNA bases 427-419"
51. .257
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58. .270
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/bound moiety= "GBV-B DNA bases 73-63"
242. .250
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156. .218
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226. .236
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|35. .154
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This invention relates to novel isolated chimeric GB virus B (GBV-B)/HCV polynucleotides. Specifically, it refers to using the hepatotropic flavivirus GBV-B that has a unique phylogenetic relationship to the human hepatitis C virus (HCV) and can serve as a surrogate virus in drug discovery efforts related to antiviral drug development. The present invention describes the construction of an infectious molecular clone current means the newly determined 3' terminal sequence of GBV-B. Furthermore, the GBV-B/HCV chimeras exhibit liver-specific expression and express HCV envelope proteins such that they can have utility as a vaccine immunogen for hepatitis C. In addition, they can be used for screening compounds certive against viral infection, as well as for developing HCV preventative and therapeutic treatments. Accordingly, these compositions exhibit virucidal, antiinflammatory and hepatotropic activities. This polynucleotide sequence is the GBV-B CDNA sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New chimeric GBV-B polynucleotide, useful as a model for hepatitis C virus, for identifying compounds active against a viral infection, or for developing hepatitis C virus preventive and therapeutic treatments.
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                                                                                      "GBV-B DNA bases 270-258"
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                                                                                                                                                                                                                                            "GBV-B DNA bases 257-251"
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/*tag= m
349. .362
/*tag= n
/bound_molety= "(
363. .384
/*tag= o
388. .394
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435. .459
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395. .406
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429. .434
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9320 CIGIGCAGAGCGIAGTACCAAGGCTGCACCCCGGTTTTTGTTCCAAGCGGAGGGAACC 9379
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50 GAGTTTGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGAT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel GB viral sequence useful in in vivo assays to identify agents which modulate hepatitis C virus activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a hepatitis GB viral-B (GBV-B) polynucleotide (see AAC91998 and AAC91996). The hepatitis GB agent was first discovered by the incculation of tamarins with serum from a patient, whose initials were GB, affected by acute hepatitis. The serum induced hepatitis in all inoculated tamarins. The present sequence comprises the sequence in AAC91998 (the 3' terminus of GBV-B, plus the JTR. This sequence confers infectivity in tamarins on otherwise non-infective GBV-B genome. This sequence is useful in in vivo assays to identify agents which modulate hepatitis C virus (HCV) activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GACGICCCITCIGGCICAICCACAAAAACCGICICGGIGGGIGAGGAGICCIGGCIGIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TGGGAAGCAGTCAGTATAATTCCCGTCGTGTGTGACGCCTCACGACGTATTTGTCCG 180
                                                                1 GAGTTTGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 CTGTGCAGAGCGTAGTACCAAGGGCTGCACCCCGGTTTTTGTTCCAAGCGGAGGGCAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GBV-B; hepatitis GB viral-B; hepatitis C virus activity; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 309 BP; 64 A; 80 C; 100 G; 65 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GBV-B 3'X sequence and 3'UTR region.
                                                                                                                                                                                                                                           9380 CCCGCTTGGAATTAAAAACT 9399
                                                                                                                                                                                                                241 CCCGCTTGGAATTAAAACT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                    ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99GB-00012432
                                                                                                                                                                                                                                                                                                                                                                  AAC92010 standard; DNA; 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 99.6
Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-061544/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200073466-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Traboni C;
                                                                                                                                                                                                                                                                                                                                                                                                            AAC92010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110
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                                                                                                                                                                                                                                                                                                                                                                                                            요. 장
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                                                                                                                              9379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a new isolated polynucleotide (I) encoding a 3' sequence of the GB virus B (GBV-B) genome, or which comprises a chimeric GBV-B genome, where at least part, but not all of a 5' nontranslated region (NTR) sequence is derived from a hepatitis C virus (HCV) 5' NTR. (I) is a GB virus B and/or hepatitis C virus polynucleotide comprising a fully defined of 260 or 2939 bp (SEQ ID NOS: 1 or 2). The polynucleotides or chimaeras are useful diagnosing or treating hepatitis C virus (HCV) and in investigating the mechanisms for the different biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        properties of the viruses. This sequence represents a Hepatitis GB virus
B (GBV-B) 3' terminal polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
    TGGGAAGCAGTCAGTATAATTCCCGTCGTGTGTGTGTGACGCCTCACGACGTATTTGTCCG
                               9260 TGGGAAGCAGTCAGTATAATTCCCGTGTGTGGTGACGCCCTCACGACGTATTTGTCCG
                                                                                                                 CTGTGCAGAGCGTAGTACCAAGGGCTGCACCCCCGGTTTTTGTTCCAAGCGGAGGGCAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New GB virus B and/or hepatitis C virus (HCV) sequences, useful in diagnosing and in treating HCV and in investigating the mechanisms the different biological properties of the viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9399 BP; 2124 A; 2322 C; 2432 G; 2521 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 260; DB 12; Length 9399; 100.0%; Pred. No. 1e-77; or Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiinflammatory; hepatotropic; virucide; GB virus B; GBV-B; hepatitis C virus; HCV; 3' terminal; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GB virus B 3' terminal polynucleotide fragment segid 2.
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                                                                                                                                                                                                CCCGCTTGGAATTAAAAACT 9399
                                                                                                                                                                        CCCCCTTGGAATTAAAAACT 260
                                                                                                                                                                                                                                                                                                                          BP.
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2000US-00587653
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(INSP ) INST PASTEUR.
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Best Local Similarity 100.6
Matches 260; Conservative
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                                                                                                                                                                                                                                                                                                                          ADJ64244 standard;
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05-JUN-2000;
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This invention relates to a novel GB virus-B (GBV-B) replicon and
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                                                                                                                                                                                                                                                                                                                                                                                                        241 CCCGCTTGGAATTAAAACT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA77752 standard; cDNA; 9397 BP.
  Claim 1; Fig 1; 81pp; English.
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446. .9040
/*tag= b
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Best Local Similarity 76.2
Matches 198; Conservative
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5'UTR
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CTGTGCAGAGCGTAGTACCAAGGGCTGCACCCCGGTTTTTGTTCCAAGCGGAGGCCAACC 240
                                             230 crerecadadestactaccadescrecaceeeerrrrrrrrrecadeegagesaace 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New GB virus B (GBV-B) replicon for identifying compounds that inhibit GBV-B or hepatitis C virus, comprises a GBV-B 5' UTR, a selection or reporter sequence, an internal ribosome entry site, an NS3-NS5B sequence, and a GBV-B 3' UTR.
                                                                                                                                                                                                    neo-RepD; GB virus-B; GBV-B; replicon; autonomous replication; NS3-NS5B; HCV; hepatitis C virus; antiviral; anti-HCV; neomycin phosphotransferase gene; neo; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                        /partial
/product= "Non structural protein 5B (NS5B)"
/note= "NS5B is an RNA dependent RNA polymerase; Start
codon is absent"
                                                                                                                                                                                    Hepatitis GB virus B subgenomic neo-RepD replicon RNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                    product= "GBV-B polyprotein NS3-NS5B"
hote= "NS= non structural protein"
1940. .7712
                                                                                                                                                                                                                                                                           /*tag= a
446. .1315
/*tag= b
/product= "Core-neo fusion protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
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                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                CCCCCTTGGAATTAAAACT 260
                                                                               290 CCCGCTTGGAATTAAAAACT 309
                                                                                                                             ADA77751 standard; RNA; 8069 BP.
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/label= IRES
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                                                                                                                                                                 20-NOV-2003
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                                                                241
                                                                                                                                                ADA77751;
                            181
                                                                                                                                                                                                                                                          Key
5'UTR
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replicon enhanced cells. A GBV-B replicon is an RNA molecule able to autonomously replicate in a cultured cell to produce detectable levels of one or more GBV-B proteins. Specifically, it may comprise the GBV-B 5.

UTR, GBV-B structural region, selection or reporter sequence, internal ribosome entry site, NS3-NS5B sequence, and GBV-B 3' UTR. Accordingly, they are useful in providing tools for studying GBV-B 19". Accordingly, they are useful in providing tools for identifying compounds that inhibit GBV-B, providing a surrogate model for identifying compounds that inhibit HCV, and providing a scaffold for producing GBV-B/HCV chimeric replicons. One to the similarity between GBV-B and the hepatitis C virus (HCV), and thibit GBV-B may be useful antiviral agents, specifically anti-HCV agents. The GBV-B subgenomic replicon constructs termed GBV-B. neo-RepA (neo-RepA), neo-RepA) neo-RepD were produced by compounds that regions coding for structural proteins and the NS2 protein with the sequences of neomyclin phosphotransferase gene (neo) and cencephalomycoarditis virus (EMCV) internal ribosome entry site (IRES) in the planmid FL3/PACYCITY. This polymorlectide sequence is the subgenomic
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/note= "From core protein to non structural protein 5B"
7268. .9040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8069 BP; 1863 A; 2075 C; 2136 G; 0 T; 1995 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.4%; Score 258.4; DB 9; Length 76.2%; Pred. No. 3.4e-77; ive 61; Mismatches 1; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to a novel GB virus-B (GBV-B) replicon and replicon enhanced cells. A GBV-B replicon is an RNA molecule able to autonomously replicate in a cultured cell to produce detectable levels of cone or more GBV-B proteins. Specifically, it may comprise the GBV-B 5.

UTR, GBV-B structural region, selection or reporter sequence, internal inclosume entry site, NS3-NS5B sequence, and GBV-B 3 UTR. Accordingly, they are useful in providing tools for studying GBV-B 1 UTR. Accordingly, they are useful in providing tools for identifying compounds that inhibit GBV-B, providing a surrogate model for identifying compounds that inhibit HC HCV, and providing a scaffold for producing GBV-B/HCV chimeric replicons. Due to the similarity between GBV-B and the hepatitis C virus (HCV), compounds that inhibit GBV-B may be useful antiviral agents, specifically arti-HCV agents. The GBV-B mbogenomic replicon constructs termed GBV-B. neo-RepB neo-RepD were produced by replacing the regions coding for structural proteins and the NS2 protein with the sequences of neomycin phosphotransferase gene (neo) and encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) in the plasmid FLJ/PACYC177. This polymucleotide sequence is the genomic GBV-B replicon cDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9138 GAGTTTGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGAT 9197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9258 IGGGAAGCAGTCAGTATAATTCCCGTCGTGTGTGTGGTGACGCCTCACGACGTACTGTCCG 9317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGGAAGCAGTCAGTATAATTCCCGTCGTGTGTGGTGACGCCTCACGACGTATTTGTCCG 180
                                                                                                                                                                                                                                                                                                                                        New GB virus B (GBV-B) replicon for identifying compounds that inhibit GBV-B or hepatitis C virus, comprises a GBV-B 5' UTR, a selection or reporter sequence, an internal ribosome entry site, an NS3-NS5B sequence,
          /partial
/product= "Non structural protein 5B (NS5B)"
/note= "NS5B is an RNA dependent RNA polymerase; start
codon is absent"
0038. .9397
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGTTTGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9397 BP; 2125 A; 2331 C; 2431 G; 2510 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9; Length 9397;
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                                                                                                                                                                                                                                                                       ΰ
                                                                                                                                                                                                                                                                       De Tomassi A, Graziani R, Paonessa G, Traboni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 99.4%; Score 258.4; DB 9, Similarity 99.6%; Pred. No. 3.6e-77; 59; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                           (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Fig 2; 81pp; English.
                                                                                                                                                                                                15-JAN-2002; 2002US-0348573P, 06-JUN-2002; 2002US-0386655P.
                                                                                                                                                                     13-JAN-2003; 2003WO-EP000281
                                                                                                                                                                                                                                                                                                  WPI; 2003-598503/56.
                                                                                                                                                                                                                                                                                                                                                                                     and a GBV-B 3' UTR
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                                                                                                               WO2003059944-A2
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les 259;
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                                                                     3'UTR
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Novel GB viral sequence useful in in vivo assays to identify agents which modulate hepatitis C virus activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGAAGCAGTCAGTATAATTCCCGTCGTGTGTGACGCCTCACGACGTATTTGTCCGC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is an isolated hepatitis GB viral-B (GBV-B) polynuclectide. The hepatitis GB agent was first discovered by the inoculation of tamarins with serum from a patient, whose initials were GB, affected by acute hepatitis. The serum induced hepatitis in all inoculated tamarins. The present sequence comprises the 3' terminus of GB-GBV-B, and confers infectivity in tamarins on otherwise non-infective GB which modulate hepatitis C virus (HCV) activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGITITGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCCATGGTCTGAAGGGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGTTTGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGATG
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                                                                                                                                                                                                                                                                                                                                                                          GBV-B; hepatitis GB viral-B; hepatitis C virus activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 259 BP; 53 A; 64 C; 81 G; 61 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 14; 76pp; English.
                                                                                                                                                                        BP.
                       9378 CCCGCTTGGAATTAAAAACT
241 CCCGCTTGGAATTAAAACT
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                                                                                                                                                                        AAC91998 standard; DNA; 259
                                                                                                                                                                                                                                                                          (first entry)
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Matches 258; Conservative
                                                                                                                                                                                                                                                                                                                         GBV-B 3'X DNA sequence
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GBV

180

for

Lemon SM, Rijnbrand R;

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New chimeric GBV-B polynucleotide, useful as a model for hepatitis C virus, for identifying compounds active against a viral infection, or developing hepatitis C virus preventive and therapeutic treatments.
        Sangar DV,
                      WPI; 2004-091362/09.
        Martin A,
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                                                                                      вв; GB virus B; GBV-B; HCV; flavivirus; hepatitis C virus; antiviral; vaccine; virucidal; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                        /*tag= k
/bound moiety= "3' terminal GBV-B RNA bases 258-252"
221. .230
/*tag= 1
/bound moiety= "3' terminal GBV-B RNA bases 250-241"
                                                                                                                                                                                             *tag= c
bound moiety= "3' terminal GBV-B RNA bases 187-186"
63. .Te6
                                                                                                                                                                                                                    *tag= d bound moiety= "3' terminal GBV-B RNA bases 184-181" (68. \ 179)
                                                                                                                                                                                                                                                       181. .184
*tag= f
/bound moiety= "3' terminal GBV-B RNA bases 166-163"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'bound_moiety= "3' terminal GBV-B RNA bases 220-214"
                                                                                                                                       152. .156
/*tag= a
/bound moiety= "3' terminal GBV-B RNA bases 199-195"
157. .160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        terminal GBV-B RNA bases 230-221"
                                                                                                                                                                             terminal GBV-B RNA bases 192-189"
                                                                                                                                                                                                                                                                                                   terminal GBV-B RNA bases 162-161"
                                                                                                                                                                                                                                                                                                                          terminal GBV-B RNA bases 160-157"
                                                                                                                                                                                                                                                                                                                                                  terminal GBV-B RNA bases 156-152"

    terminal sequence of the hepatitis GB virus B RNA SeqID 1.

                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                           /*tag= g
/bound_moiety= "3'
189. .192
                                                                                                                                                                     *tag= b
bound moiety= "3'
61. .162
                                                                                                                                                                                                                                                                                                                   *tag= h
bound_moiety= "3'
                                                                                                                                                                                                                                                                                                                                          *tag= i
'bound_moiety= "3'
:01. .212
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/bound_moiety= "
252. .258
                        ADJ56731 standard; RNA; 260 BP.
                                                                                                                                                                                                                                                                                                                                                                 /*tag= j
/label= SL-2
214. 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-2003; 2003WO-US021002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUL-2002; 2002US-00189359
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label= SL-1
                                                                                                                                                                                                                                             *tag= e
label= SL-3
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                                                       (first entry)
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                                                                                                               Hepatitis GB virus B.
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                                                       06-MAY-2004
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                                        ADJ56731;
        RESULT 8
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This invention relates to novel isolated chimeric GB virus B (GBV-B)/HCV polynucleotides. Specifically, it refers to using the hepatotropic flavivirus GBV-B that has a unique phylogenetic relationship to the human hepatitis C virus (HCV) and can serve as a surrogate virus in drug discovery efforts related to antiviral drug development. The present invention describes the construction of an infectious molecular clone using the newly determined 3' terminal sequence of GBV-B. Furthermore, the GBV-B/HCV chimeras exhibit liver-specific expression and express HCV envelope proteins such that they can have utility as a vaccine immunogen for hepatitis C. In addition, they can be used for screening compounds certive against viral infection, as well as for developing HCV preventative and therapeutic treatments. Accordingly, these compositions exhibit virucidal, antiinflammatory and hepatotropic activities. This polynoric contents are successived.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12; Length 260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.8%; Score 254.4; DB 12; Length
75.8%; Pred. No. 2.3e-76;
tive 61; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB virus B 3' terminal polynucleotide fragment seqid 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 260 BP; 53 A; 63 C; 82 G; 0 T; 62 U; 0 Other;
Example 1; SEQ ID NO 1; 108pp; English.
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| CUUGGAAUUAAAACU 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 75.8*
Matches 194; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the invention.
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Hepatitis G virus.
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                                                                                                                                                                                                         The invention describes a new isolated polynucleotide (I) encoding a 3' sequence of the GB virus B (GBV-B) genome, or which comprises a chimeric GBV-B genome, where at least part, but not all of a 5' nontranslated region (NTR) sequence is derived from a hepatitis C virus (HCV) 5' NTR. (I) is a GB virus B and/or hepatitis C virus polynucleotide comprising a fully defined of 260 or 9399 bp (SEQ ID NOS: 1 or 2). The polynucleotides or chimaeras are useful disquosting or treating hepatitis C virus (HCV) and in investigating the mechanisms for the different biological properties of the viruses. This sequence represents a Hepatitis GB virus B (GBV-B) 3' terminal polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis G virus; GBV-C; anti-HIV; human immunodeficiency virus; AIDS; infectious GB virus type C; acquired immunodeficiency syndrome; GBV-B; fatigue; fever; swollen gum; leston; constipation; diarrhoea; seizure; opportunistic infection; Kaposi's sarcoma; skin rash; loss of appetite; headache; speech impairment; muscle atrophy; memory loss; pain; diplopia; cold intolerance; anxiety; groin lump; pruritus; genital sore; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 TCCCTTCTGGCTCATCCACAAAACCGTCTCGGGTGGGTGAGGAGTCCTGGCTGTGTGGG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 AAGCAGTCAGTATAATTCCCGTCGTGTGTGGTGACGCCTCACGACGTATTTGTCCGCTGT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New GB virus B and/or hepatitis C virus (HCV) sequences, useful in diagnosing and in treating HCV and in investigating the mechanisms for the different biological properties of the viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAGAGCGUAGUACCAAGGCUGCACCCCGGUUUUUGUUCCAAGCGGAGGGCAACCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGAGCGTAGTACCAAGGGCTGCACCCCGGTTTTTGTTCCAAGCGGAGGCCAACCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                             5 TTGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCCATGGTCTGAAGGGGATGACG
                                                                                                                                                                                                                                                                                                                                                                                        Gabe
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                                                                                                                                                                                                                                                                                                                                                            97.8%; Score 254.4; DB 12; Length 260; 75.8%; Pred. No. 2.3e-76; ive 61; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3' nontranslated region (ntr) of hepatitis G virus (GBV-B)
                                                                                                                                                                                                                                                                                                                                         Sequence 260 BP; 53 A; 63 C; 82 G; 0 T; 62 U; 0 Other;
                                                                                          Rijnbrand
                                                                                                                                                                                                                                                                                                                  (GBV-B) 3' terminal polynucleotide.
                                                                                                                                                                                   Claim 2; SEQ ID NO 1; 58pp; English.
                                                                                          Lemon SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS15946 standard; RNA; 362 BP
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244 CUUGGAAUUAAAACU 259
                     04-JUN-1999; 99US-0137665P.
03-JUL-2002; 2002US-00189359
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                                                      TEXAS SYSTEM.
PASTEUR.
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Best Local Similarity 75.8
Matches 194; Conservative
                                                                                          Sangar DV,
                                                                                                              WPI; 2004-203294/19.
                                                      (TEXA ) UNIV
(INSP ) INST
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                                                                                          Martin A,
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The invention relates to an isolated and purified nucleic acid molecule

(I) encoding an infectious GB virus type C (GBV-C) (also known as heartleid of virus (HGV). (I) is useful in a method for proparing an infectious GBV-C. (I) is useful for inhibiting human immunodeficiency virus (HIV) disease infection or progression (acquired immunodeficiency syndrome (AIDS)) in a subject, or for inhibiting a cell aspecially CD4+cell or an animal preferably human, infected with HIV. A reduction in everity or progression of AIDS includes, but is not limited to prevention of or a reduction in the severity, duration, or discomfort associated with the following conditions: prolonged and unexplained actique, swollen glands, prolonged fever, chills, excessive sweating, swollen gums and lesions, sore throat, shortness of breath, constipation, diarrhoea, symptoms of well-known opportunistic infections. Kaposi's arcomas, skin rashes, loss of appetite or weight loss, malaise, headaches, speech impairment, muscle atrophy, memory loss, swelling of the joints, cold intolerance, pain or tenderness in bones, energy level, anxiety, stress, and tension, groin lump, pruritus, genital sores,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag= n
note= "Forms double-stranded region with bases 11 to 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotide encoding an infectious GB virus type C useful as vaccine for inhibiting human immuno virus disease infection or progression in a
                                                                              double-stranded region with bases 362 to
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Location/Qualifiers
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                                         /*tag= a
/note= "Forms of 352"
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27-NOV-2000; 2000US-0253390P.
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111. 130
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352. .362
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320. 335
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which modulate hepatitis C virus (HCV) activity
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                                                                                   94.4%;
ilarity 75.7%;
Conservative 61
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/*tag= b
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                                                                                                      cal Similarity
196; Conserv
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                                                                                   Query Match
                                                                                                        Best Local
Matches 19
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                                                                                                                                                                                                                                                                                                                                       120
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    blurred or decreased vision, diplopia, light sensitivity, pain, and seizures. (I) can be used to produce a polypeptide, preferably an antigen which is useful for producing an immune response in a subject or for use as a vaccine. The present sequence represents the 3 nontranslated region
                                                                                                                                                                                                                                                                           60 GAGUUUGGCGACCAUGGUGGAUCAGAACCGUUUCGGCUGAAGCCAUGGUCUGAAGGGGGAU 119
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                                                                                                                                                                    DB 5; Length 362;
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                                                                                                                                                                  Query Match
Best Local Similarity 73.5%; Pred. No. 2.1e-74;
Matches 191; Conservative 62; Mismatches 7; Indels
                                                                                                                              Sequence 362 BP; 78 A; 87 C; 102 G; 0 T; 95 U; 0 Other;
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                                                                                       of hepatitis G virus (GBV-B)
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Best Local
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                                                                                                                                                                                                              61 ACGUCCCUUCUGGCUCAUCCACCAAAAACC-UCUCGGGUGGGUGAGGAGUCCUGGCUGUGU
                                                                                                                                                                                                                                                                                                                                                                1 AGUTUGGCGACCAUGGUGGAUCAGAACCGUTUCGGGUGAAGCCAUGGUCUGAAGGGAUG
                                                                                                                                                                                                                                                                                        182 TGTGCAGAGGGTAGTACCAAGGGCTGCACCCCGGTTTTTGTTCCAAGCGGAGGGCAACCC
                                                                                                                  2 AGTITGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGATG
                                                                                                                                                                                                                                                                    122 GGGAAGCAGTCAGTATAATTCCCGTCGTGTGGTGACGCCTCACGACGTATTTGTCCGC
                                                                             Gaps
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                                                                             7
                                          Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GBV-B;
                                                                             1; Indels
Sequence 258 BP; 53 A; 64 C; 80 G; 0 T; 61 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GB virus B 3' terminal polynucleotide fragment #1.
                                          DB 4;
                                        Score 245.4; DB 4
Pred. No. 2.7e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rijnbrand
                                                                             61; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiinflammatory; hepatotropic; virucide; hepatitis C virus; HCV; 3' terminal; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lemon SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGCTTGGAATTAAAAACT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
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The invention describes a new isolated polynucleotide (I) encoding a 3' sequence of the GB virus B (GBV-B) genome, or which comprises a chimeric GBV-B genome, where at least part, but not all of a 5' nontranslated region (NTR) sequence is derived from a hepatitis C virus (HCV) 5' NTR. (I) is a GB virus B and/or hepatitis C virus polynucleotide comprising a fully defined of 260 or 3939 bp (SEQ ID NOS: 1 or 2). The polynucleotides or chimaeras are useful diagnosing or treating hepatitis C virus (HCV) and in investigating the mechanisms for the different biological properties of the viruses. This sequence represents a Hepatitis GB virus B (GBV-B) 3' terminal polynucleotide. Note: This sequence represents nucleotides 152-259 of the sequence shown in ADJ64243.
                                                                                                                                                                                                                                                                                                                                      153 TGGTGACGCCTCACGACGTATTTGTCCGCTGTGCAGAGCGTAGTACCAAGGGCTGCACCC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  viral sequence useful in in vivo assays to identify agents which hepatitis C virus activity.
                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is an isolated hepatitis GB viral-B (GBV-B) polynuclectide. The hepatitis GB agent was first discovered by the incoulation of tamarins with serum from a patient, whose initials were GB, affected by acute hepatitis. The serum induced hepatitis in all incoulated tamarins. The present sequence comprises the 3' terminus of
                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                            213 CGGTTTTTGTTCCAAGCGGAGGGCAACCCCCGGCTTGGAATTAAAAACT 260
                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 41.5%; Score 108; DB 12; Length 108; Local Similarity 76.9%; Pred. No. 1.7e-26; ne 83; Conservative 25; Mismatches 0; Indels C
                                                                                                                                                                                                                                 Seguence 108 BP; 23 A; 30 C; 30 G; 0 T; 25 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 19 A; 23 C; 23 G; 0 T; 17 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 4; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GBV-B; hepatitis GB viral-B; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC92012 standard; RNA; 82 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99GB-00012432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAY-2000; 2000WO-EP004622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GBV-B 3'X RNA sequence #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-061544/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                       Matches
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This invention relates to novel isolated chimeric GB virus B (GBV-B)/HCV polynucleotides. Specifically, it refers to using the hepatotropic flavivirus GBV-B that has a unique phylogenetic relationship to the human to hepatitis C virus (HCV) and can serve as a surrogate virus in drug cliscovery efforts related to antiviral drug development. The present invention describes the construction of an infectious molecular clone invention describes the construction of an infectious molecular clone the GBV-B/HCV chimeras exhibit liver-specific expression and express HCV envelope proteins such that they can have utility as a vaccine immunogen for hepatitis C. In addition, they can be used for screening compounds for hepatitis C. In addition, as well as for developing HCV chimeras and therapeutic treatments. Accordingly, these compositions exhibit virucidal, antiinflammatory and hepatotropic activities This course and a mutagenic PCR primer used to amplify the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New chimeric GBV-B polynucleotide, useful as a model for hepatitis C virus, for identifying compounds active against a viral infection, or for developing hepatitis C virus preventive and therapeutic treatments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTACCAAGGGCTGCACCCCGGTTTTTGTTCCAAGCGGAGGGCAACCCCCCGCTTGGAATTA 254
CGCTGTGCAGAGCGTAGTACCAAGGGCTGCACCCCGGTTTTTGTTCCAAGCGGAGGGCAA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 GTACCAAGGGCTGCACCCCGGTTTTTGTTCCAAGCGGAGGGCAACCCCCGCTTGGAATTA 49
                Mutagenic PCR primer used to amplify hepatitis GB virus B cDNA SeqID 12.
                                                                                                                                                                                                                                                                                                                          88; GB virus B; GBV-B; HCV; flavivirus; hepatitis C virus; antiviral;
vaccine; virucidal; antiinflammatory; PCR; primer; mutagenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.4%; Score 66; DB 12; Length 108; llarity 100.0%; Pred. No. 3.7e-12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 108 BP, 23 A, 33 C, 30 G; 22 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rijnbrand R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 22; SEQ ID NO 12; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GBV-B cDNA sequence of the invention.
                                                                   CCCCCCCTTGGAATTAAAACT 260
                                                                                                  82
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                                                                                     |||||||||::||||::|||||:
                                                                                                                                                                       742/c
ADJ56742 standard; DNA; 108 BP.
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(INSP ) INST PASTEUR.
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                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis GB virus B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004005498-A1
                                                                                                                                                                                                                                                           06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
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                                                                                                                                                                                                                             ADJ56742;
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Matches
                                                                                                                                                         RESULT 14
                                                                                                                                                                             ADJ56742/
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Gaps

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Query Match 31.5%; Score 82; DB 4; Length 82; Best Local Similarity 79.3%; Pred. No. 1.1e-17; Matches 65; Conservative 17; Mismatches 0; Indels

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The invention describes a new isolated polynucleotide (I) encoding a 3' sequence of the GB virus B (GBV-B) genome, or which comprises a chimeric GBV-B genome, where at least part, but not all of a 5' nontranalated region (NTR) sequence is derived from a hepatitis C virus (HCV) 5' NTR. (I) is a GB virus B and/or hepatitis C virus polynucleotide comprising a fully defined of 260 or 9399 bp (SEQ ID NOS: 1 or 2). The polynucleotides or chimaeras are useful diagnosting or tracting hepatitis C virus (HCV) and in investigating the mechanisms for the different biological properties of the viruses. This sequence represents a primer used in the construction of a Hepatitis GB virus B (GBV-B) infectious clone.
                                                                                                                                                                                                                                                                          antiinflammatory; hepatotropic; virucide; GB virus B; GBV-B;
hepatitis C virus; HCV; 3' terminal; primer; ss; PCR; infectious clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New GB virus B and/or hepatitis C virus (HCV) sequences, useful in diagnosing and in treating HCV and in investigating the mechanisms for the different biological properties of the viruses.
                                                                                                                                                                                                                                        Hepatitis GB virus B infectious clone related primer segid 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.4%; Score 66; DB 12; Length 108; Best Local Similarity 100.0%; Pred. No. 3.7e-12; Matches 66; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 108 BP; 23 A; 33 C; 30 G; 22 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lemon SM, Rijnbrand R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 22; SEQ ID NO 12; 58pp; English
                                                                                                    255 AAAACT 260
                                48 AAAACT 43
                                                                                         RESULT 15
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195 GTACCAAGGGCTGCACCCCGGTTTTTGTTCCAAGCGGAGGGCAACCCCCGCTTGGAATTA 254 108 GTACCAAGGGCTGCACCCCGGTTTTTGTTCCAAGCGGAAGGGCAACCCCCGCTTGGAATTA 49 255 AAAACT 260 g ઠે ઠ

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0; Gaps

Search completed: December 7, 2005, 21:08:27 Job time: 370 seca

48 AAAACT 43

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December 7, 2005, 13:50:44; Search time 127 Seconds (without alignments) 3639.103 Million cell updates/sec
                                                                                                                                                                                                                                                                                       1 gagtttggcgaccatggtgg.......cccgcttggaattaaaaact 260
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2: /cgn2 6/ptodata/1/ina/5 COMB.seq:*
3: /cgn2 6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2 6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2 6/ptodata/1/ina/H.COMB.seq:*
6: /cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
7: /cgn2 6/ptodata/1/ina/PP.COMB.seq:*
8: /cgn2 6/ptodata/1/ina/PP.COMB.seq:*
9: /cgn2 6/ptodata/1/ina/PP.COMB.seq:*
9: /cgn2 6/ptodata/1/ina/PP.COMB.seq:*
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Compugen Ltd.
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Copyright (c) 1993 - 2005
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query

No. Score Match Length DB ID

1 258.4 99.4 309 3 US-09-579-302-1

2 257.4 99.0 259 3 US-09-579-302-3

4 257.4 99.0 259 3 US-09-579-302-4

5 257.4 99.0 259 3 US-09-579-302-4

6 82 31.5 82 3 US-09-579-302-4

7 30.8 11.8 133356 3 US-09-579-302-4

8 30.8 11.8 133356 3 US-09-579-302-4

9 30.4 11.7 2044 3 US-09-949-016-12651 Sequence 16.64, Appli Sequence 17.64, A

TGGGAAGCAGTCAGTATAATTCCCGTCGTGTGTGGTGACGCCTCACGACGTATTGTCCG 180

121 170 181 230

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CTGTGCAGAGGGTAGTACCAAGGGCTGCACCCGGTTTTTGTTCCAAGCGAAGGGAACC 240

11.2 1723 2 US-07-901-703-10 Sequence 10, Appl 11.2 1723 2 US-08-147-023-28 Sequence 3, Appl 11.2 1723 2 US-08-206 644-3 Sequence 3, Appl 11.2 1723 2 US-08-278-729A-20 Sequence 3, Appl 11.2 1723 2 US-08-480-528A-7 Sequence 20, Appl 11.2 1723 2 US-08-480-528A-7 Sequence 7, Appl 11.2 1723 2 US-08-155-343A-20 Sequence 20, Appl 11.2 1723 2 US-08-155-343A-20 Sequence 20, Appl 11.2 1723 2 US-08-451-553A-20 Sequence 20, Appl 11.2 1723 2 US-08-451-50A-7 Sequence 20, Appl 11.2 1723 2 US-08-441-670A-7 Sequence 20, Appl 11.2 1723 2 US-08-441-670A-7 Sequence 20, Appl 11.2 1723 2 US-08-411-084-20 Sequence 20, Appl 11.2 1723 2 US-08-411-084-20 Sequence 20, Appl 11.2 1723 2 US-08-412-088-20 Sequence 20, Appl 11.2 1723 3 US-08-41	ALIGNMENTS 1. Application US/09579302 atent No. 6527437 ENERAL INFORMATION: ENERAL INFORMATION: APPLICANT: Trabon1, Cinzia TITLE OF INVENTION: No. 6627437el GBV sequence FILE REFREENCE: Mewburn CURRENT APPLICATION NUMBER: US/09/579,302 CURRENT FILING DATE: 2000-05-25 PRIOR APPLICATION NUMBER: GB 9912432.3 NUMBER OF SEQ ID NOS: 16 SOFTWARE: PATENT NOS: 16 EQ ID NO 1 EQ ID NO 1 EXTRE: DNA ORGANISM: GBV-B-like virus FRATURE: DNA	KEY: 3'UTR ION: (1)(309) INFORMATION: COMplementary to the last 49 published 3'UTR INFORMATION: DONA complementary to the last 49 published 3'UTR INFORMATION: nucleotides of GBV-B plus a novel nucleotide (C) INFORMATION: in position 44 and 259 novel nucleotide sequence INFORMATION: at the 3' end.	h Similarity 99.6%; Pred. No. 8.2e-81; 59; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	GAGTITIGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGAT 60 	GACGTCCCTTCTGGCTCATCCACAAAACCGTCTCGGGTGAGGAGAGAGTCCTGGCTGTG 120
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 Sequence 1, Applicat Patent No. 6627437 GENERAL INFORMATION: APPLICANT: Traboni, TITLE OF INVENTION: FILE REFERENCE: New FURRENT APPLICATION CURRENT APPLICATION CURRENT PILING DATE PRIOR APPLICATION PRIOR PELING DATE NUMBER OF SEQ ID NO SOFTWARE: PATENTIN LENGTH: 309 TYPE: DNA CORGANISM: GBV-B-li PERTURE:	PETITIONS INCAPITORS INCAPITORS INCAPITORS OTHER INFORMS OTHER INFORMS OTHER INFORMS OTHER INFORMS	Matc Local	1 GAC 	61 GAC 10 GAC
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-09-57; Sequent; GENERA APPLIA FITE CURRE; CURRE; PRIOR SOFTW SCO ID SCO ID LENG	0 - S	Query M Best Lo Matches	è 8	රු සි

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241 CCGCTTGGAATTAAAAACT 259
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                                                                                                                                                                                                                                                                                             19 ccccrrccaarraaaacr 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: GBV-B-like virus
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US-09-579-302-5/c
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US-09-579-302-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 TGTGCAGAGCGTAGTACCAAGGGCTGCACCCCGGTTTTTGTTCCAAGCGGAGGCCAACCC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGUUUGGCGACCAUGGUGGAUCAGAACCGUUUCGGGUGAAGCCAUGGUCUGAAGGGGAUG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGAAGCAGTCAGTATAATTCCCGTCGTGTGTGTGACGCCTCACGACGTATTTGTCCGC
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99.0%; Score 257.4; DB 3;
Best Local Similarity 76.1%; Pred. No. 1.7e-80;
Matches 197; Conservative 61; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.0%; Score 257.4; DB 3; 99.6%; Pred. No. 1.7e-80; ive 0; Mismatches 1;
                                                                                                  Sequence 2, Application US/09579302
Patent No. 6627437;
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Traboni, Cinzia
TITLE OF INVENTION: No. 6627437el GBV sequence
FILE REFERENCE: Weaburn
CURRENT APPLICATION NUMBER: US/09/579,302
CURRENT FILING DATE: 2000-05-25
FRIOR APPLICATION NUMBER: GB 9912432.3
PRIOR PAPLICATION NUMBER: GB 9912432.3
PRIOR FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 2
LENGTH: 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Traboni, Cinzia
TITLE OF INVENTION: No. 6627437el GBV sequence
FITLE OF INVENTION: No. 6627437el GBV sequence
FILE REFERENCE: Mewburn
CURRENT APPLICATION NUMBER: US/09/579,302
CURRENT FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: GB 9912432.3
PRIOR FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Pacentin Ver. 2.1
SEQ ID NO 3
LENGTH: 259
                           290 cccccrrccaarraaaacr 309
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Patent No. 6627437
                                                                                                                                                                                                                                                                                                                            TYPE: RNA
; ORGANISM: GBV-B-like virus
US-09-579-302-2
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ORGANISM: GBV-B-like virus
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Best Local Similarity 99.6
Matches 258; Conservative
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259 AGITIGGCGACCAIGGIGGATCAGAACCGTTTCGGGTGAAGCCAIGGTCTGAAGGGGATG 200
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                                                                                                  122 GGGAAGCAGTCAGTATAATTCCCGTCGTGTGTGGTGACGCCTCACGACGTATTTGTCCGC 181
                                                                                                                                                                                                                                                 TGTGCAGAGCGTAGTACCAAGGGCTGCACCCCGGTTTTTGTTCCAAGCGGAGGGCAACCC 241
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                                                                                                                                                                                                      80
61
                                                                                                                                                                                                                                                                      2 AGITITGGCGACCAIGGIGGAICAGAACCGIIITCGGGIGAAGCCAIGGICIGAAGGGGAIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOCATION: (1)...(259)
CTHER INFORMATION: CDNA Of positive strand 3'UTR of GBV-BUS-09-579-302-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09579302

Patent No. 6627437
GENERAL INFORMATION:
FILE REFERENCE: Mewburn
CURRENT FILING DATE: 2000-05-25
PRIOR FILING DATE: 1999-05-27
PRIOR FILING DATE: 1999-05-27

PRIOR FILING DATE: 1999-05-27

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 4

LENGTH: 259
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Sequence 12651, Application US/09949016
; Sequence 12651, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANTY VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REFERENCE: CLOOD1307
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-04-14
; PRIOR PLILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTHARE: FREESEQ for Windows Version 4.0
; SEQ ID NO 12651
; LEMORTH: 133360
                                                                                                                                                        RESULT 7

US-09-949-016-16964

i Sequence 16964, Application US/09949016

j Patent No. 6812339

i GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

PILER REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR PAPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,768

PRIOR PELING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
11.8*; Score 30.8; Di
Best Local Similarity 55.7*; Pred. No. 11;
Matches 59; Conservative 0; Mismatches
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11.8%; Score 30.8; D
Best Local Similarity 55.7%; Pred. No. 11;
Matches 59; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16964
LENGTH: 133358
                                               239 CCCCCCCTTGGAATTAAAACT 260
                                                                       61 CCCCGCUUGGAAUUAAAACU 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Human
US-09-949-016-16964
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US-09-949-016-12651
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; ORGANISM: Human
US-09-949-016-12651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 GGGAAĞCAGTCAĞTATAATTCCCGTCĞTĞTĞTĞTĞACĞCCTCACGACGTACTTGTCCĞC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 TGTGCAGAGCGTAGTACCAAGGGCTGCACCCCGGTTTTTGTTCCAAGCGGAGGCCAACCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 TGTGCAGAGCGTAGTACCAAGGGCTGCACCCCGGTTTTTGTTCCAAGCGGAGGGCAACCC
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                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: 3'UTR
COCATION: (1)..(259)
COTHER ION: (1)..(259)
CHER PRORMATION: cDNA of negative strand 3'UTR of GBV-B
US-09-579-302-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.0%; Score 257.4; DB 3; Best Local Similarity 99.6%; Pred. No. 1.7e-80; Matches 258; Conservative 0; Mismatches 1;
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31.5%; Score 82; DB 3; Le
Best Local Similarity 79.3%; Pred. No. 5.2e-19;
Matches 65; Conservative 17; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TILE OF INVENTION: No. 6627437el GBV sequence FILE REFERENCE: Mewburn CURRENT APPLICATION NO. 6627437el GBV sequence; CURRENT APPLICATION NUMBER: US/09/579,302 CURRENT FILING DATE: 2000-05-25; PRIOR FILING DATE: 1999-05-27 NUMBER OF SEQ ID NOS: 16; SEQ ID NO 14 LENGTH: 82
                     Patent No. 6627437
GENERAL INFORMATION:
TITLE OF INVENTION:
CURRENT FABOUT.
CURRENT APPLICATION NUMBER: US/09/579,302
CURRENT FILING DATE: 2000-05-25;
PRIOR FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 5:
LENGTH: 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/09579302
Patent No. 6627437
GENERAL INFORMATION:
Sequence 5, Application US/09579302
Patent No. 6627437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 CCGCTTGGAATTAAAAACT 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: RNA; GBV-B-like virus
US-09-579-302-14
                                                                                                                                                                                                                                                                                                                                                  ORGANISM: GBV-B-like virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
US-09-579-302-14
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Length 601;

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APPLICANT: ALA-KOKKO, LEENA, et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
NUMBER OF SEQUENCES: 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 TGTGGTGACGCCTCACGACGTATTTGTCCGCTGTGCAGAGCGTAG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CUNTRY: USA

ZIF: 19103-7086

ZIF: 19103-7086

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: PASTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,731
FILING DATE: 03-0CT-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/212,322
FILING DATE: 14-MAR-1994
PRIOR APPLICATION NUMBER: US 07/803,628
FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION: KATHRYN
NAME: DOYLE LEARY PI.D., KATHRYN
NAME: DOYLE LEARY PI.D., KATHRYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C. STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET,
                                                                                                                                                                                                                                                                                                              DB 3;
                                                                                                                                                                                                                                                                                                      Score 29.8; DE
Pred. No. 2.6;
0; Mismatches
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 182173
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: PROCKOP, DARWIN J.
APPLICANT: SPOTILA, LORETTA D.
APPLICANT: BELTAS, CONSTANTINOS
APPLICANT: BEREDA, LARLSA
APPLICANT: LARSON, ANDREA W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-943-731-3/c
; Sequence 3, Application US/08943731
; Patent No. 6265157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET UNDBER: 95
TELECOMMUNICATION INFORMATION
TELEPHONE: 215-965-1284
                                                                                                                                                                                                                                                                                                          11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COLIGE, ALAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 831-494
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                     58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PACK, MICHAEL
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CITY: PHILADELPHIA
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 58; Conserv
                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-182173
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APPLICANT:
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APPLICANT:
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TELEX: 8
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| Sequence 182173, Application US/09949016
| Patenn No. 6812339
| Patenn No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| CURRENT FILING DATE: 2000-04-14
| PRIOR PELLING DATE: 2000-10-20
| PRIOR PELLING DATE: 2000-10-03
| PRIOR PELLING DATE: 2000-10-03
| PRIOR PELLING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15750, Application US/09949016

Sequence 15750, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REPERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PRILOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0
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LOCATION: (1)...(20444)
OTHER INFORMATION: n = A,T,C or G
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Matches 76, Conservative
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US-09-949-016-15750
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LENGTH: 20444
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APPLICANT: Gould-Rothberg, Bonnie

TITLE OF INVENTION: Method of Identifying a Psychotropic Agent Using
TITLE OF INVENTION: Differential Gene Expression

FILE REFERENCE: 1596-519

CURRENT APPLICATION NUMBER: US/09/468,253B

CURRENT FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: 60/113,127

PRIOR FILING DATE: 1998-12-21

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin Ver. 2.1
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US-09-468-253B-51/c
Sequence 51, Application US/09468253B
Patent No. 6750012
GENERAL INFORMATION:
TITLE OF INVENTION: Method of Identifying a Psychotropic Agent Using
TITLE OF INVENTION: Differential Gene Expression
FILE REFERENCE: 15966-519
CURRENT APPLICATION NUMBER: US/09/468,253B
CURRENT FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: 60/113,127
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                                                                                                                           Length 24183;
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Pred. No. 4.5;
0; Mismatches 96; Indels 5
                                                                                                                                                                    Indels
                                                                                                                                                                    52;
                                                                                                                           11.5%; Score 29.8; DB 3; 54.0%; Pred. No. 12;
                                                                                                                                                                    0; Mismatches
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US-09-468-253B-53/c
; Sequence 53, Application US/09468253B
; Patent No. 6750012
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECTLE TYPE: DNA (genomic)
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Best Local Similarity 50.2%;
Matches 102; Conservative (
                                                                                                                                            Best Local Similarity 54.08
Matches 61; Conservative
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LENGTH: 1002
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US-08-943-731-3
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US-09-468-253B-61/c
US-09-468-253B-61/c
Sequence 61, Application US/09468253B
Patent No. 6750012
GENERAL INFORMATION:
TITLE OF INVENTION: Method of Identifying a Psychotropic Agent Using
TITLE OF INVENTION: Differential Gene Expression
FILE REFERENCE: 1596-519
CURRENT APPLICATION NUMBER: US/09/468,253B
CURRENT FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: 60/113,127
PRIOR FILING DATE: 1998-12-21
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11.3%; Score 29.4; DB 3;
Best Local Similarity 50.2%; Pred. No. 4.5;
Matches 102; Conservative 0; Mismatches 96;
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11.3%; Score 29.4; DE
Best Local Similarity 50.2%; Pred. No. 4.6;
Matches 102; Conservative 0; Mismatches
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PRIOR FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 51
LENGTH: 1005
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 61
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US-09-468-253B-61
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US-09-468-253B-62/c
; Sequence 62, Application US/09468253B
; Patent No. 6750012
; Patent No. 6750012
; Patent No. 6750012
; APPLICANT: Gould-Rothberg, Bonnie
; TITLE OF INVENTION: Method of Identifying a Psychotropic Agent Using
; TITLE OF INVENTION: Differential Gene Expression
; TITLE OF INVENTION: Differential Gene Expression
; FILE REFERENCE: 15966-519
; CURRENT APPLICATION NUMBER: US/09/468,253B
; CURRENT APPLICATION NUMBER: 60/113,127
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIN Ver. 2.1
; SEQ ID NO 62
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Best Local Similarity 50.2%; Pred. No. 4.6;
Matches 102; Conservative 0; Mismatches 96; Indels 5.
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CORGANISM: Mus musculus
US-09-468-253B-62
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Sequence 551953,
Sequence 31040, A
Sequence 425967,
Sequence 487889,
Sequence 66, Appl
Sequence 66, Appl
Sequence 5423, Ap
Sequence 5423, Ap
Sequence 5423, Ap
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Sequence 2, Appli
Sequence 12, Appli
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Sequence 132082,
Sequence 132082,
Sequence 425966,
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
                                                                                    7, 2005, 17:19:59; Search time 535 Seconds (without alignments) 4018.763 Million cell updates/sec
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Sequence 1,
Sequence 2,
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1: /cgn2_6/ptodata/1/pubpna/USO1_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO3_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO3B_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO3B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO3B_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO3B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO3B_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USO3B_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO3B_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO3B_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO3B_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-189-359-2

US-10-501-412-1

US-10-189-359-1

US-10-189-359-12

US-10-189-359-12

US-10-189-359-12

US-10-027-632-132082

US-10-027-632-132082

US-10-027-632-132082

US-10-027-632-132082

US-10-027-658-45966

US-11-097-143-31040

US-11-097-143-31040

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US-10-267-502-86
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US-11-097-143-5423
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US-11-097-143-5422
US-10-972-079-75557
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                                                                                                                                                                                                                                                           9793542 seqs, 4134689005 residues
                                                                                                                                           US-10-009-002-1_COPY_9140_9399
260
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                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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Sequence 27988, A Sequence 27988, A Sequence 160056, Sequence 8625, Ap Sequence 81927, A Sequence 110, App Sequence 110, App Sequence 1110, App Sequence 214, App Sequence 21455, Sequence 21623, A Sequence 85459, A Sequence 86202, A Sequence 9, Appli Sequence 1, Appli
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US-10-972-079-75558
US-10-027-632-27988
US-10-027-632-27988
US-10-425-114-22247
US-10-425-115-160056
US-10-425-115-160056
US-10-425-115-161927
US-10-029-386-25170
US-10-491-472-80
US-10-367-057-170
US-10-887-057-170
US-10-489-740-91
US-10-425-115-141545
US-10-425-115-141545
US-10-425-115-141545
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US-10-425-115-141545
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US-11-013-314-9
US-11.097-143-21022
US-10-329-670-1
US-10-158-865-1
US-10-981-687-1
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                                                                                                                                                                                                                                                                                                                                      USGUENCE 1, Application US/09742659
Sequence INFORMATION:
APPLICANT: Hong, Zhi
APPLICANT: Butkiewicz, Nancy J.
APPLICANT: Ingravallo, Paul
APPLICANT: Hong, Weidong
APPLICANT: Lemon, Stanley M.
TITLE OF INVENTION Stanley M.
TITLE OF INVENTION Chimeric HCV/GBV-B viruses
FILE REFERENCE: ID01116
CURRENT APPLICATION NUMBER: US/09/742,659
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 16
SEQ ID NOS: 16
SEQ ID NO 1
LENGTH: 9399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 6.2e-82;
Matches 260; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                           ALIGNMENTS
 11.5 600
11.5 724
11.5 1482
11.3 309
11.3 348
11.3 1467
11.3 1463
11.3 4638
11.3 1497
11.3 1642
11.2 1003
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ORGANISM: GB virus-B
  US-09-742-659-1
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CTGTGCAGAGGGTAGTACCAAGGGCTGCACCCGGTTTTTGTTCCAAGCGGAGGGCAACC

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SEQ ID NO 2
LENGTH: 9397
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US-10-501-412-1
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                                                              TYPE: RNA
                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9260 TGGGAAGCAGTCAGTATAATTCCCGTCGTGTGTGGTGACGCCTCACGACGTATTTGTCCG 9319
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| Publication No. US20050239205A1
| GENERAL INFORMATION:
| APPLICANT: De Tomasal, Amedeo
| APPLICANT: De Tomasal, Amedeo
| APPLICANT: De Tomasal, Amedeo
| APPLICANT: Tranboni, Cinzia
| TITLE OF INVENTION: BNHANCED CELLS
| FILE REPERENCE: 1TR00374P US/10/501,412
| CURRENT APPLICATION NUMBER: DCT/EP03/00281
| PRIOR FILING DATE: 2002-06-06
| PRIOR PAPLICATION NUMBER: 60/386,655
| PRIOR PAPLICATION NUMBER: 60/386,655
| PRIOR PAPLICATION NUMBER: 60/348,573
| PRIOR FILING DATE: 2002-01-15
| PRIOR FILING DATE: 2002-01-15
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                                                                                                                                Sequence 2, Application US/10189359
Publication No. US20040039187A1
GENERAL INFORMATION:
APPLICANT: MARTIN, Annette
APPLICANT: SANGAR, DAVID V.
APPLICANT: LEMON, STANLEY M.
TITLE OF INVENTION: CHIMETIC GB Virus B (GBV-B); FILE REFERENCE: UTSG:258US
CURRENT APPLICATION NUMBER: US/10/189,359
FRIOR PRICOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 2.
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 260; DB 7; Best Local Similarity 100.0%; Pred. No. 6.2e-82; Matches 260; Conservative 0; Mismatches 0;
                              9380 CCCGCTTGGAATTAAAACT 9399
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241 CCCGCTTGGAATTAAAAACT 260
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; ORGANISM: GBV-A-like virus
US-10-189-359-2
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                                                                                                                              99.4%; Score 258.4; DB 9; Length 8069; 76.2%; Pred. No. 2.2e-81; ive 61; Mismatches 1; Indels 0;
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 8069
                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||::|||||:
8050 CCCGCUUGGAAUUAAAAACU 8069
                                                                                                                                                                                                                                                                                                                                                                                                                            CCCCCTTCCAATTAAAACT 260
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US-10-501-412-2
                                                                                       OTHER INFORMATION: GBV-B Replicon
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                                                          ORGANISM: Artificial Sequence
                                                                                                                                Query Match
Best Local Similarity 76.2*
Matches 198; Conservative
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48 AAAACT 43
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                                                             9258 TGGGAAGCAGTCAGTATAATTCCCGTCGTGTGTGTGACGCCTCACGACGACGTACTTGTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Unknown Organism: GB VIRUS US-10-189-359-1
                                                                                                                                                                                                                                                      Sequence 1, Application US/10189359
Publication No. US20040039187A1
GENERAL INFORMATION;
APPLICANT: MARTIN, Annette
APPLICANT: SANGAR, DAVID V.
TITLE OF INVENTION; STANLEY M.
TITLE REPRENCE: UTS6:258U5
CURRENT APPLICATION NUMBER: US/10/189,359
CURRENT FILLING DATE: 2002-07-03
PRIOR FILLING DATE: 2002-07-03
NUMBER: OF SEQ ID NOS: 16
SOFTWARE: PATENTIN VET: 2.11
                                                                                                                                                                              9378 CCGCTTGGAATTAAAAACT 9397
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Publication No. US20040039187A1
GENERAL INFORMATION:
                                                                                                                                                           CCCGCTTGGAATTAAAAACT 260
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244 CUUGGAAUUAAAACU 259
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APPLICANT: SANGAR, DAVID V.
APPLICANT: LEMON, STANLEY M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Unknown
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US-10-189-359-12/c
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LENGTH: 260
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US-10-189-359-1
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APPLICANT: YUE, Henry
APPLICANT: YUE, Henry
APPLICANT: YUE, Mondique G.
APPLICANT: YAO, Mondique G.
APPLICANT: YAO, Mondique G.
APPLICANT: TANG, Y. Tom
APPLICANT: TANG, Y. Tom
APPLICANT: RHAN, Farrah A.
TITLE OF INVENTION: FARRANCE: PT-0005 PCT
CURRENT APPLICATION NUMBER: US/10/168,651
CURRENT APPLICATION NUMBER: 60/172,000; 60/176,083; 60/177,332; 60/178,572; 60/179,758
FIGH APPLICATION NUMBER: 20/172,000; 60/176,083; 60/177,332; 60/179,758
FIGH APPLICATION NUMBER: 20/172,000; 60/176,083; 60/177,332; 60/179,758
FIGH APPLICATION NUMBER: 60/172,000; 60/176,083; 60/177,332; 60/179,758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 GTACCAAGGGCTGCACCCCGGTTTTTGTTCCAAGCGAGGGCAACCCCCGCTTGGAATTA 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-189-359-12
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12.3%; Score 32; DB 6; Length 3179;
Best Local Similarity 50.7%; Pred. No. 1.5;
Matches 77; Conservative 0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030171275A1 3232992CB1
US-10-168-651-36
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
25.4%; Score 66; DB 7; Length 108
Best Local Similarity 100.0%; Pred. No. 4.5e-13;
Matches 66; Conservative 0; Mismatches 0; Indels
TITLE OF INVENTION: Chimeric GB Virus B (GBV-B); FILE REFERENCE: UTSG:258US; CURRENT APPLICATION NUMBER: US/10/189,359; CURRENT FILING DATE: 2002-07-03; PRIOR APPLICATION NUMBER: .10/189,359; PRIOR FILING DATE: 2002-07-03; NUMBER OF SEQ ID NOS: 16; SEQ ID NOS: 16; SEQ ID NO 12; LENGTH: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36, Application US/10168651
Publication No. US20030171275A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YANG, Jumming
REDDY, Roopa
LAL, Preeti
HILLWAM, Jennifer L.
AZIMZAI, Yalda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAUGHN, Mariah R.
BURFORD, Neil
AU-YOUNG, Janice
LU, Dyung Aina M.
                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-02-10
NUMBER OF SEQ ID NOS: 54
SOFTWARE PERL Program
SEQ ID NO 36
LENGTH: 3179
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens US-09-925-065A-425966
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US-10-027-632-132082
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                                                                                                     2836 GAGCATTGTCCAAGCTGGCTCTTGGGGGGTCCCCCATTGGCCACAAGGCCTCACCCCCCCA 2777
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                                                                                                                                                                                                                 70 TCTGGCTCATCCACAAAACCGTCTCGGGTGAGGAGTCCTGGCTGTGTGGGAAGCA 129
GACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGATGACGTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417 ACCAAGGAACTTAGGGAGGTGAAGTCATTTCTGGGTGGGAGATCATCCTGTCAAGGGTG
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Publication No. US20030204075A9
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION, NUMBER: US 60/198,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5; Length 645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification and Mapping of Single North Title OF INVENTION: Identification and Mapping of Single North Title OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/128,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR APPLICATION NUMBER: US 60/165,363
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-09-28
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/166,002
PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2716 GGGGCTAAGCTCCCCAAAGCGGGTTGGGGC 2685
                                                                                                                                                                                                                                                                                                                                                                                                                                       130 GTCAGTATAATTCCCGTCGTGTGTGTGACGC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.2%; Score 31.8; Cilarity 54.8%; Pred. No. 1.2; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 132082
LENGTH: 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 132082, Application US/10027632; Publication No. US20020198371A1; GENERAL INFORMATION:
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Best Local Similarity
Matches 63; Conserv
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US-10-027-632-132082
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US-09-925-065A-425966

Sequence 425966, Application US/09925065A

Publication No. US20050228172A9

Sequence 425966, Application US/09925065A

Publication No. US2005028172A9

SEGUENCE INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

PRICE REPERENCE:

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2000-10-08-08

PRIOR PELING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/260,092

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-05-09

INWHERE OF SEQ ID NOS: 957086

SOFTWARE: FeatSEQ for Windows Version 4.0

LENGTH 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52; Indels
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Pred. No. 1.6;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31.8; DB
Pred. No. 1.2;
0; Mismatches
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PASECEC FOR WINDOWS VERSION 4.0
SEQ ID NO 132082
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Best Local Similarity 52.8%;
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.2%;
Best Local Similarity 54.8%;
Matches 63; Conservative
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740 ercrargiardiaiadeicegesegadadadadegegesegacadadaadiaadaaageg
680 AİTTITİDAĞĞCICTAÇÇAÇATAGACATAİCATĞCTAĞAATĞTGTGTĞTĞTĞTĞTĞT 739
                                                                                                                                                                     124 GAAGCAGTCAGTATAATTCCCGTCGTGTGGTGACGCCTCACGACGTATTTGTCCGCTG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 GCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGATGACGTCC 67
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLBIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLO00728
                                                                          64 GICCCTICTGGCTCATCCACAAAAACCGTCTCGGGTGGGTGAGGAGTCCTGGCTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR PELING DATE: 2000-11-20
PRIOR PPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2010-05-09
NUMBER OF SEQ ID NOS: 957066
SOFTWARE: FEALSEQ for Windows Version 4.0
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Pred. No. 3.7;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATATGGATGACAGATAAACACCCTGTGGCGAG 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 CTICIGGCICATCCACAAAACCGICICGGGIG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-0925-065A-551953
Sequence 551953, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 31040, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 58.1
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                    800 GGAGGACTGGA 810
                                                                                                                                                                                                                                                                        184 TGCAGAGCGTA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
US-09-925-065A-551953
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TITLE OF INVENTION: METHODS AND REAGENTS FOR IDENTIFYING RARE FETAL CELLS IN THE MATE
TITLE OF INVENTION: CIRCULATION
FILE REFERENCE: 11012-004-99
CURRENT APPLICATION NUMBER: US/10/818,168
CURRENT FILING DATE: 2004-04-05
PRIOR PELLING DATE: 2004-04-11-15
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                             RESULT 11
US-10-000-897-36
Sequence 36, Application US/10000897
Publication No. US20030165852A1
Sequence 36, Application US/10000897
Publication No. US20030165852A1
GENERAL INFORMATION:
TITLE OF INVENTION: MATERNAL CIRCULATION
FILLE REFERENCE: 11012-004-999
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/248,882
PRIOR APPLICATION NUMBER: 60/248,882
PRIOR PILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 GAAGCAGTCAGTATAATTCCCGTCGTGTGTGACGCCTCACGACGTATTTGTCCGCTG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 TITGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCCATGGTCTGAAGGGGGATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.9%; Score 31; DB 6; Length 1095; Best Local Similarity 47.6%; Pred. No. 2.6; Matches 91; Conservative 0; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8; Length 1095;
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Best Local Similarity 47.6%; Pred. No. 2.6;
Matches 91; Conservative 0; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 36, Application US/10818168 Publication No. US20040185495A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 TGCAGAGCGTA 194
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CORGANISM: Homo sapiens
US-10-818-168-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
              225 CAA 227
                                                           122 TAA 124
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LENGTH: 1095
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4 TTTGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGATGAC 63

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 AGGCGCTGAAGTCCTGGCTGACTGAAACGAACAAGCCGTTCGCGGCACGTGTTGAGTTCG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AGGCCACTGGAACTGAGCCCACCGCTGCCAGTGGAACACTGCACGAGTGGTTATGCCTC. 61
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Publication No. US20050228172A9

FURINGER INFORMATION:
TITLE OF INVENTION: Unclectide Polymorphisms in the Human Genome TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome FILE REFERENCE: 108627.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

FRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-20

FRIOR FILING DATE: 2000-11-30

FRIOR FILING DATE: 2001-01-4

FRIOR FILING DATE: 2001-01-6

FRIOR APPLICATION NUMBER: US 60/250,092

FRIOR APPLICATION NUMBER: US 60/261,766

FRIOR APPLICATION NUMBER: US 60/261,766

FRIOR APPLICATION NUMBER: US 60/261,766

FRIOR APPLICATION NUMBER: US 60/261,766

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FRIOR APPLICATION NUMBER: US 60/261,766

FRIOR APPLICATION NUMBER: US 60/261,766

FRIOR APPLICATION NUMBER: US 60/280,846

FRIOR FILING DATE: 2001-01-16

FRIOR FILING DATE: 2001-05-09

NUMBER: PASSEQ for WINGOWS VERSION 4.0

FRIOR FILING DATE: 201-05-09

NUMBER: FASSES FOR FOR WINGOWS VERSION 4.0
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11.6%; Score 30.2; DB 4; Length 645;
Best Local Similarity 52.8%; Pred. No. 4.4;
Matches 65; Conservative 0; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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11.8%; Score 30.6; DB 10;
Best Local Similarity 58.1%; Pred. No. 4.9;
Matches 54; Conservative 0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 GGCTGTGTGGGAAGCAGTCAGTATAATTCCCGT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 crcrcaaccrarccaciccircacircccr 165
                FRIOR AFFLING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-11-22
PRIOR FILING DATE: 1999-11-22
PRIOR FILING DATE: 1999-11-28
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 2000-01-12
PRIOR PLING DATE: 2000-01-12
PRIOR FILING DATE: 2000-02-34
PRIOR FILING DATE: 2000-02-34
PRIOR FILING DATE: 2000-02-34
PRIOR FILING DATE: 2000-03-33
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: PRESEQ FOR WINDOWN VERBION 4.0
SEQ ID NO 31040
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; ORGANISM: Homo sapiens
US-09-925-065A-425967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: DROSOPHILA
US-11-097-143-31040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-09-925-065A-425967
PRIOR
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165 ACGACGTATTTGTCCGCTGTGCAGAGCGTAGTACCAAGGGCTGCACCCCGGTTTTTGTTC 224

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Db 62 GCCAAGTGTGTGTGTGTGGGGCTTACCATCACCTGCTACTCCCTTCCCTGTGC 121

Oy 225 CAA 227

Db 122 TAA 124

Search completed: December 7, 2005, 20:59:42

Job time: 539 Becs
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US-11-051-568-28
RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 28, Appl
Sequence 26, Appl
Sequence 63, Appl
Sequence 63, Appl
Sequence 63, Appl
                                                                            7, 2005, 19:43:05; Search time 146 Seconds (without alignments) 665.769 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                               | cgn2 6/prodata/2/pubpna/US09 NEW PUB.seq:*
| cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*
| cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*
| cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
| cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*
| cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*
| cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq2:*
| cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq2:*
| cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq2:*
| cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq3:*
| cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq3:*
             5.1.6
Compugen Ltd.
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US-11-165-53296

US-11-1052-544-28

US-11-051-568-26

US-11-101-086-59

US-11-121-086-63

US-11-121-086-63

US-10-750-185-3299

US-10-750-185-3299

US-10-750-185-3299

US-10-750-185-3491

US-10-750-185-3491

US-10-750-185-3491

US-10-750-185-3491

US-10-750-185-3650

US-10-750-185-3650

US-10-750-185-3650

US-10-750-185-3650

US-10-750-185-3650

US-10-750-185-3650

US-10-750-185-3650
                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                        3392430 seqs, 186927314 residues
                                                                                                                                                                                                                                                                                                                                    Published Applications NA New:*
                                                                                                                        US-10-009-002-1_COPY_9140_9399
260
1 gagtttggcgaccatggtgg.......
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              GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                         nucleic search, using sw model
                                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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1413
4539
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1699
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319608
38703
1926
162537
169725
200628
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255.8
255.8
25.6
6
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Perfect
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No.
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; TYPE: DNA
; ORGANISM: Bovine 19866880574203
US-10-750-185-53296
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Best Local Similarity 64.2%;
KERR, Richard
ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43; Conservative
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LENGTH: 1660
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OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
/product= "hOP2-PP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 11.2%; Score 29; DB 7; Length 1723; Best Local Similarity 55.4%; Pred. No. 1.4; Matches 56; Conservative 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 867 gasárrccscriraaccrgacccagarcccogcigosogogo 907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: DIANA M. STEEL
REGISTRATION NUMBER: 43,153
REFERENCE/DOCKET NUMBER: STK-001CP6C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEPAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1723 base pairs
                   APPLICATION NUMBER: US 07/810,560
FILING DATE: 20-DEC-1991
APPLICATION NUMBER: US 07/669,920
FILING DATE: 20-DEC-1990
APPLICATION NUMBER: US 07/600,024
FILING DATE: 18-OCT-1990
APPLICATION NUMBER: US 07/616,374
FILING DATE: 18-OCT-1990
APPLICATION NUMBER: US 07/616,374
FILING DATE: 22-FEB-1990
APPLICATION NUMBER: US 07/179,406
FILING DATE: 22-FEB-1990
APPLICATION NUMBER: US 07/179,406
FILING DATE: 15-AUG-1988
APPLICATION NUMBER: US 07/22,630
FILING DATE: 15-AUG-1988
APPLICATION NUMBER: US 07/216,630
FILING DATE: 15-EB-1991
APPLICATION NUMBER: US 07/422,699
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,699
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,699
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,699
FILING DATE: 17-OCT-1989
APPLICATION NUMBER: US 07/422,693
FILING DATE: 17-OCT-1989
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /notes "hop2 (cDNA)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-11-051-568-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
TISSUE TYPE: HIPPOCAMPUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
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%3-10-750-185-53296/c
%Sequence 53296, Application US/10750185
%Publication No. US20050260603A1
GENERAL INFORMATION:
% APPLICANT: MMI GENOMICS, INC.
% APPLICANT: DeNISE, Sue K.

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Sequence 1, Application US/11145703

Publication No. US2050260667A1

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marta

APPLICANT: Bunuenfeld, Marta

APPLICANT: Batlouk, Laurent

APPLICANT: Batlouk, Laurent

APPLICANT: Batlouk, Laurent

APPLICANT: Batlouk, Laurent

APPLICANT: Batlouk, Laurent

TITLE OF INVENTION: SCHIZOPHERNIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS

FILE REFERENCE: 53.USL6.DIV.

CURRENT APPLICATION NUMBER: US/11/145,703

CURRENT APPLICATION NUMBER: US 60/126,903

PRIOR FILING DATE: 2000-03-30

PRIOR PLILNG DATE: 1999-03-30

PRIOR PLILNG DATE: 1999-07-14

PRIOR PLILNG DATE: 1999-07-14

PRIOR PLILNG DATE: 1999-07-14

PRIOR APPLICATION NUMBER: US 60/145,915

PRIOR PLILNG DATE: 1999-07-14

PRIOR PLILNG DATE: 1999-07-14

PRIOR PLILNG DATE: 1999-07-14

PRIOR PLILNG DATE: 1999-07-14

PRIOR PLILNG DATE: 1999-07-14

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PRIOR PLILNG DATE: 1999-07-14

PRIOR PLILNG DATE: 1999-07-14

PRIOR PLILNG DATE: 1999-07-14

PRIOR PLING DATE: 1999-07-14

PRIOR PLILNG DATE: 1999-07-14

PRIOR PLING DATE: 1999-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 TGCAGAGCGTAGTACCAAGGCCTGCACCCCGGTTTTTGTTCCAAGCGGAGGGCAACCCCC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 TGCAGAGGGGAGCAGCTCATGCTACAGCCAGATCTAGGTTCAAACCGGAATCCACCACC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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NUMBER OF SEQ ID NOS: 234
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1660;
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
TITLE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28.6; Di
Pred. No. 1.9;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1
LENGTH: 319608
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FEATURE:
NAME/KEY: exon
LOCATION: 240528..240569
OTHER INFORMATION: exon M1117 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEBRUSKEY: exon
LOCATION: 240528..240596
OTHER INFORMATION: exon M1090 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: exon
COCATION: 240528..240617
STHER INFORMATION: exon M1069 complement g34872 gene
                NAME/KEY: exon
LOCATION: 216661..216952
OTHER INFORMATION: exon Qbis complement 934872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: exon
LOCATION: 231272..231412
OTHER INFORMATION: exon Obis complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IAME/KEY: exon
CCCATION: 217406..237428
OTHER INFORMATION: exon Nbis complement g34872 gene
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LOCATION: 240528..240824
OTHER INFORMATION: exon M862 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
COCATION: 246528..240994
CHTER INFORMATION: exon M692 complement g34872 gene
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: exon
LOCATION: 240528..240644
OTHER INFORMATION: exon MS2 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: exon
LOCATION: 231787..231880
OTHER INFORMATION: exon O2 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: exon
ACCATION: 231870..231879
MTHER INFORMATION: exon Ol complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: exon
LOCATION: 239719..239807
JTHER INFORMATION: exon N2 complement 934872 gene
                                                                                                                                                                                                   NAME/KEY: exon
LOCATION: 217027..217061
OTHER INFORMATION: exon Q1 complement g34872 gene
                                                                                    FEATURE:
NAME/KEY: exon
LOCATION: 216661..217061
OTHER INFORMATION: exon Q complement g34872 gene
                                                                                                                                                                                                                                                                                             NAME/KEY: exon
LOCATION: 229647..229742
OTHER INFORMATION: exon X complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 230408..230721
OTHER INFORMATION: exon P complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME,KEY: exon
LOCATION: 234174..234321
OTHER INFORMATION: exon O complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 239719..239853
OTHER INFORMATION: exon N complement g34872 gene
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LOCATION: 215819..215975
OTHER INFORMATION: exon Rbis complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AME/KEY: misc feature
OCATION: 65854..67854
OTHER INFORMATION: 3'regulatory region g35018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: 213818..215818
OTHER INFORMATION: 3'regulatory region g34872 gene
                        PEATURE:
NAME/KEY: misc_feature
LOCATION: 31..1107
OTHER INFORMATION: 5'regulatory region g35018 gene
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JTHER INFORMATION: exon R complement g34872 gene
                                                                                                                                                                                                                                                                                                                       NAME/KEY: exon
LOCATION: 18778..18862
OTHER INFORMATION: exon Bbis 935018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
ACCATION: 29967...30282
WHER INFORWATION: exon E g35018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
OCATION: 64666..64812
OTHER INFORMATION: exon F 935018 gene
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COCATION: 65505..65853
OTHER INFORMATION: exon G 935018 gene
                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: exon
LOCATION: 25593..25740
OTHER INFORMATION: exon C g35018 gene
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COCATION: 29388..29502
OTHER INFORMATION: exon D g35018 gene
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LOCATION: 214676..214793
JTHER INFORMATION: exon T 935030 gene
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LOCATION: 215702..215746
JTHER INFORMATION: exon U 935030 gene
                                                                                                                                                                                                                                NAME/KEY: exon
LOCATION: 14877..14920
JTHER INFORMATION: exon B 935018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: exon
LOCATION: 201188..201234
JTHER INFORMATION: exon S 935030 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 216836..216915
OTHER INFORMATION: exon V 935030 gene
                                                                                                                                                        LOCATION: 1108..1289
OTHER INFORMATION: exon A 935018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCATION: 94124..94964
THER INFORMATION: exon 935017
ORGANISM: Homo sapiens
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US20050255141A1
  Publication No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15869 IGTGGGTTCAGTATTGAACATCAATGCTACTGTGTGTGTGAGTCCTAGTATTGCCAGCTGCA 15928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 GGGTGAAGCCATGGTCTGAAGGGGATGACGTCCTTCTGGCTCATCCACAAAACCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                               Query Match
11.0%; Score 28.6; DB 7; Length 319608;
Best Local Similarity 55.6%; Pred. No. 11;
Matches 55; Conservative 0; Mismatches 44; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.5%; Score 27.4; DB 7; Length 38703; Best Local Similarity 50.4%; Pred. No. 14; Matches 67; Conservative 0; Mismatches 66; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence; note OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28, Application US/11052544
| Fublication No. US2005025504A1
| GENERAL INFORMATION:
| APPLICANT: PARL, FILE F.
| TITLE OF INVENTION: METHOD OF DETECTING AN INCREASED | TITLE OF INVENTION: SUSCEPTIBILITY TO BREAST CANCER | FILE REFERENCE: 22000.0127U2 | CURRENT APPLICATION NUMBER: US/11/052,544 | FILE RPPLICATION NUMBER: 60/543,866 | PRIOR APPLICATION NUMBER: 60/543,866 | PRIOR APPLICATION NUMBER: 05.404-02-12 | NUMBER OF SEQ ID NOS: 29 | SOFTWARE: FastSEQ for Windows Version 4.0 | SEQ ID NO 28 | LENGTH: 33703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21505 caddrigacrdaadrrdrdarrdarrigaaradracrca 21543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 CGGGTGGGTGAGGAGTCCTGGCTGTGTGGGAAGCAGTCA 133
                                                                                                                                                                    FEATURE: NAME/KEY: misc feature LOCATION: 241686..243685 OTHER INFORMATION: 5'regulatory region g34872 gene
                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
LOCATION: 290652..292652
OTHER INFORMATION: 3'regulatory region g34665 gene
                                                                                                                                                  complement g34872 gene
                         LOCATION: 240528..241685
OTHER INFORMATION: exon M1 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-11-051-568-26
; Sequence 26, Application US/11051568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15929 rccercerca 15941
                                                                                                                         LOCATION: 240800..240993
OTHER INFORMATION: exon MS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 TCCGCTGTGCAGA 189
                                                                                               NAME/KEY: exon
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                         ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
GENERAL INFORMATION:

APPLICANT: OPPERMANN, HERMANN
OZKAYTAK, ENGIN
KUBERASAMPTH, THANGAVEL
RUEGER, DAVID C.
PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: 10/321,799
FILING DATE: 17-DEC-2002
APPLICATION NUMBER: US 09/148,925
FILING DATE: 8-SEP-1998
APPLICATION NUMBER: US 08/449,699
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: US 08/147,023
APPLICATION NUMBER: US 07/841,646
FILING DATE: 1-NOV-1993
APPLICATION NUMBER: US 07/841,646
FILING DATE: 28-7M-1992
APPLICATION NUMBER: US 07/821,052
APPLICATION NUMBER: US 07/579,865
FILING DATE: 7-SEP-1990
APPLICATION NUMBER: US 07/521,849
FILING DATE: 4-DEC-1990
APPLICATION NUMBER: US 07/621,949
FILING DATE: 4-DEC-1990
APPLICATION NUMBER: US 07/621,949
FILING DATE: 4-DEC-1990
APPLICATION NUMBER: US 07/621,949
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FILING DATE: 22-FEB-1990
APPLICATION NUMBER: US 07/179,406
FILING DATE: 08-APR-1988
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APPLICATION NUMBER: US 07/422,699
FILING DATE: 17-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/810,560
FILING DATE: 20-DEC-1991
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FILING DATE: 20-AUG-1990
APPLICATION NUMBER: US 07/600,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/599,543
FILING DATE: 18-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/232,630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/315,342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 23-FEB-1989
APPLICATION NUMBER: US 07/660,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/11/051,568
FILING DATE: 04-Feb-2005
CLASSIFICATION: <URKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/616,374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 18-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 21-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 15-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                        STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02110
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1
                                                                                                                                                                                                                                                                                                               CITY: BOSTON
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Gaps

ö

29; Indels

; Score 26.6; DB ; Pred. No. 44; 0; Mismatches

10.2%;

DB 7; Length 169725;

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74 GCTCATCCACAAAAACCGTCTCGGGTGGGTGAGGAGTCCTGGCTGTGGGAAGCAGTCA
          APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REPERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT APPLICATION NUMBER: US/11/121,086
PRIOR PILLING DATE: 2005-05-04
PRIOR FILLING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SEQ ID NO 63
LENGTH: 169725
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.3%
                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                US-11-121-086-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401 gageriregreaacargergaacgegeceaccergeceraccagagecacacacresaa 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAGTITGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 TGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGGATGACGTCCCTTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 59, Application US/11121086
Publication No. US2005026645941
EMBERRAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138.6000-000000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
NUMBER OF FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 27.2; DB 7; Length 162537; Pred. No. 27; 0; Mismatches 23; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1926;
                                                                                                                                                                                                                                                                                                                    /function= "OSTEOGENIC PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 caccircricacricarcaranancicarricacing 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 7;
REFERENCE/DOCKET NUMBER: STK-001CP6C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.5%; Score 27.2; D
Best Local Similarity 53.8%; Pred. No. 6.1;
Matches 56; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-121-086-63
; Sequence 63, Application US/11121086
; Publication No. US20050266459A1
                  TELECOMMUNICATION INFORMATION
                                 TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1926 base pairs
                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 93..1289
OTHER INFORMATION: /
/product="moP2-PP"
/note="moP2-CDNA"
                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.5%;
                                                                                                                                                                                                                                         TISSUE TYPE: EMBRYO
                                                                                                                                                                                                                      ORGANISM: MURIDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 64.1<sup>3</sup>
Matches 41, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CORGANISM: Homo sapiens
US-11-121-086-59
                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51442 CCCA 51445
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TRNGTH: 162537
                                                                                                                                                                                                                                                                                                                                                                                                      US-11-051-568-26
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US-11-121-086-59
                                                                                                                                                                                                                                                                FEATURE
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64410 GCTTGGGCACACCAGCGTCTGAAGTGTGTGTGGGCCCCCTGCCAGCGTGGTTAGCAGACA 64351
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                                                                                                                                                                                                     US-11-121-086-62/c

Sequence 62, Application US/11121086

Sequence 62, Application US/11121086

Sequence 62, Application US/11121086

GENERAL INFORMATION:

APPLICANT: NELESN, KIRSTEN V.

TILE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

FILE REFERENCE: 09138.6000-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT APPLICATION NUMBER: 2005-05-04

PRIOR FILING DATE: 2004-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 200628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
10.2%; Score 26.6; DE
Best Local Similarity 60.3%; Pred. No. 46;
Matches 44; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NS-10-750-185-58438/C
; Sequence 58438, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: DMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.3
SEQ ID NO 62
LENGTH: 200628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64350 GAGCTGCTGCCCT 64338
                                                                                                      16690 caccrecreccer 16702
                                                        134 GTATAATTCCCGT 146
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US-11-121-086-62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 CCATGGTCTGAAGGGGATGACGTCCCTTCTGGCTCATCCACAAAACCGTCTCGGGTGGG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 TCCTGGCTGTGTGGGAAGCAGTCAGTATAATTCCCGTCGTGTGTGACGCCTCACGAC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 TCAGGGCAGAGTGGGAAGCAGTGGGTTTCAGTTCCTTGGTGTCTGGGTCCTCATTGGGA 225
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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MI GENOMICS, INC.
APPLICANT: KERR, Richard
APPLICANT: KERR, Richard
APPLICANT: APPLICANT: Source
APPLICANT: KERR, Richard
APPLICANT: APPLICANT: ROSENFELD, David
APPLICANT: APPLICANT: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
## APPLICANT: HOLM, Tom
### APPLICANT: BATES, Stephen
### APPLICANT: BATES, Stephen
### APPLICANT: PANTIN, Dennis
### TITLE OP INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
### TITLE OP INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
### CURRENT APPLICATION NUMBER: US/10/750,185
### CURRENT PILING DATE: 2003-12-31
### PRIOR PILING DATE: 2002-12-31
### NUMBER OF SEQ ID NOS: 64922
### SEQ ID NO 58438
### LENGTH: 1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
10.2%; Score 26.4; DB 6; Length 1683;
Best Local Similarity 59.2%; Pred. No. 11;
Matches 45; Conservative 0; Mismatches 31; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 2078;
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Best Local Similarity 59.2%; Pred. No. 12;
Matches 45; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Bovine 19866880696449
US-10-750-185-32595
                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Bovine 19866880937133
US-10-750-185-58438
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SOFTWARE: Patentin version 3.1
SEQ ID NO 32595
LENGTH: 2078
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; Sequence 109, Application US/11102240 ; Publication No. US20050260647A1

RESULT 11 US-11-102-240-109

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APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
TYLE ON GOGOWSKI, Paul L.
TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS
TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS
TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS
FILE REFERENCE: P2330R10106667
FRICK APPLICATION NUMBER: 10/063667
FRICK APPLICATION NUMBER: PCT/US00/23328
FRICK FILING DATE: 2001-12-06
FRICK APPLICATION NUMBER: 60/170262
FRICK FILING DATE: 199-12-09
NUMBER OF SEQ ID NOS: 170
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| Publication No. US20050260603A1
| GENERAL INFORMATION:
| APPLICANT: WING GENOMICS, INC.
| APPLICANT: EXER. Richard
| APPLICANT: EXER. Richard
| APPLICANT: EXER. Richard
| APPLICANT: HOLM, Tom
| APPLICANT: HOLM, Tom
| APPLICANT: HOLM, Tom
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| APPLICANT: HOLM, Tom
| APPLICANT: HOLM, Tom
| HOLMS APPLICATION NUMBER: US/10/750,185
| CURRENT FILING DATE: 2003-12-31
| HOUMER OF SEQ ID NOS: 64922
| COFFWARE: PATENTIN VERBION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.1%; Score 26.2; DB 6; Length 1267; Best Local Similarity 63.5%; Pred. No. 12; Matches 40; Conservative 0; Mismatches 23; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 26.4; DB 7;
Pred. No. 12;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 GCTGTGTGGGAAGCAGTCAGTATAATTCCCGT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 828 GCCGTGTGCTAAGAAGTGATGGCAAGACTTGT 859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.2%;
Best Local Similarity 55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-750-185-39628/c
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APPLICANT:
APPLICANT:
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Sequence 2422, Application US/10750185

Subjication No. US2005026603A1

GENERAL INFORMATION:

APPLICANT: MI GENOMICS, INC.

APPLICANT: ROSENFELD, David

APPLICANT: ROSENFELD, David

APPLICANT: RATEN, Techan

APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MM1100-2

CURRENT PLING DATE: 2003-12-31

FRIOR APPLICATION NUMBER: US 60/437,482

PRIOR FILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 2422

SEQ ID NO 2422

SEQ ID NO 2422

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SEQ ID NO 2422
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APPLICANT: MIGGENORICS, INC.
APPLICANT: MIGGENORICS, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFRENCE: MAIL100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
FRIOR PELLOR DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 39518
LENGTH: 1431
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Pred. No. 12;
0; Mismatches 18;
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                                                                                                                                               Sequence 39518, Application US/10750185
Publication No. US20050260603A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Bovine 19866880359182
US-10-750-185-39518
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Best Local Similarity 67.3%;
Matches 37; Conservative
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ORGANISM: Bovine MMBT15901
                                          1169 GGG 1167
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US-10-750-185-39518/c
72 TGG 74
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APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILLOO-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                                                                            Sequence 24904, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MHI GENOMICS, INC.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bovine 19866880791951
US-10-750-185-24904
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SOFTWARE: Patentin version 3.1
SEQ ID NO 24904
LENGTH: 1032
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Local Similarity 59.5%;
hes 44; Conservative
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                                                                                   138 AATTCCCGTC 147
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CA216674 SCCCST3C1 BUB15456 AGBNCOURT BIB57875 603388443 CX122717 NMB00585 AL657400 AL857400 AG577493 MUB MUBCU AG57743 Jul mubcu AG559170 MUB MUBCU

BU339106 603515968

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Sequence:

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GSS; genome survey sequence; MICER.

Mus musculus (house mouse)

SM Mus musculus (house mouse)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Muroidea; Murinae; Rodentia;

Sciurognathi; Muroidea; Murinae; Mus.

E. 1 (bases 1 to 657)

S. Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,

Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,

Rogers, J. and Bradley, A.

Direct Submission

L. Submitted (20-PEB-2004) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                                                                                                               BX964816
Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN287p06, genomic survey sequence.
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llarity 54.8%; Pred. No. 11;
Conservative 0; Mismatches
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/ol_type="genomic DNA"
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/clone="WHPN287p06"
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CA216674
BU915456
BU915456
BU877475
CX122717
AGS77493
CO051243
AGS59170
BU339106
ALS68674
BB50470
CX52248
CD780119
CN178451
BB303397
BB421037
CC64446
CC764446
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BU162131
CN804856
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  Query Match
Best Local S:
Matches 69
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BX964816/c
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AL347370 Tetracdon
CO738666 SILEG4C21
ALG72732 ALG72732
BQ919900 AGENCOURT
BEG15183 601281124
BG6157472 602639444
CV242705 WS02515.B
AV072177 AV072177
BP744242 BP74442
AG65743 Pan trogl
AG118154 Pan trogl
BQ931612 AGENCOURT
BB425694 BB425694
BB825694 BB425694
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AZ962384 2M0231L11
                                                                              7, 2005, 20:50:41; Search time 2435 Seconds (without alignments) 4995.746 Million cell updates/sec
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                                                                                                                                                  gagtttggcgaccatggtgg.........cccgcttggaattaaaaact 260
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Compugen Ltd.
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260
             GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
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                                                         nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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DB seq length: 200000000
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Match Length DB
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CK525779 r8wfa0 00 BB385246 BB385246 BM691308 UI-E-CII-CR840902 GR0AAA9DH

BB807696 CK525779 BB385246 BM691308 CR840902

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314 254 254

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

DEFINITION

RESULT 2 AZ962384

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Murinae, Mus.

Sciurognathi, Muroidea, Muridae, Murinae, Mus.

1 (bases 1 to 818)

Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Elect Submission

Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
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Tetraodon nigroviridis genome Burvey sequence T7 end of clone
045G18 of library A from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                              CR247935 Brand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN90111, genomic survey sequence.
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194 AGTACCAAGGGCTGCACCCCGGTTTTTGTTCCAAGCGGAGGCCAACCCCCCGCTTGGAATT 253
                                            411 AAAATGAAGATAGCCCTCAGGTGTTGTAACGAATGAATGGAAACCACATGTGGGAAAA 470
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Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus
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AL347370.1 GI:8241140
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Best Local Similarity 54.8<sup>†</sup>
Matches 69; Conservative
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CR247935/c
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Bab. Female. (John Strain XL10-Gold, T1-resistant, F-" (210ne 11b="Mouse 10kb plasmid UUGC2M library" (210ne 11b="Mouse 10kb plasmid UUGC2M library" (210ne 11b="Wouse 10kb plasmid UUGC2M library" (Mouse "Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (Eemale) was obtained from the Jackson Laboratory Mouse DNA Resources (John Female). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynerses and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis vector DNA was prepared from a derivative of phasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                     AZ962384 670 bp DNA linear GSS 27-APR-2001 2M0231L11F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0231L11 F, genomic survey sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchoncoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0231 row: L column: 11
Seg primer: CGTYGTAAAACGACGCCAGT
Class: plasmid ends
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/mol_type="genomic DNA"
strain="CS7B1/6J"
/db_xref="taxon:10090"
/clone="UUGCM0231L11"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 670.
Location/Qualifiers
                                                                                                                                                                                                                                 Mus musculus (house mouse)
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Fax: 801 585 7177
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Matches 69; Conserv
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84112, USA
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Achaptus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

El (bases 1 to 571)
Songer Xenopus; Silurana.

El (bases 1 to 571)
Songer Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
AL On Sep 15, 2002 this sequence version replaced g1:22892997.

Con Sep 15, 2002 this sequence version replaced g1:22892997.

Con Sep 15, 2002 this sequence version replaced g1:22892997.

Con Sep 15, 2002 this sequence version replaced g1:22892997.

Email: trop@sanger.ac.uk
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS ESCUENCE ID: TEggl35n13.plkSP6
Sequencing primer: 5P6
Sequencing primer: 5P6
Sequencing primer: 5P6
Constructed by Aaron M. Zorn.

Constructed by Aaron M. Zorn.

CDNA was oligo dT primed from Sug of poly A+ RNA from egg.
ECORI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.
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AL872732 XGC-egg Xenopus tropicalis cDNA clone TEgg135n13 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 TGGCTCATCCACAAAACCGTCTCGGGTGAGGAGTCCTGGCTGTGGGAAGCAGT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="embryo"
/dev_stage="embryonic"
/lab_host="B.coli Electromax DH10B"
/clone_llb="squirrel embryo library 1"
/note="Vector: pFLC; Site 1: Sali GTCGAG; Site_2: BamHI
/GGATCC; Normalized and subtracted cDNA library prepared
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 72B
Tel: +44(0)151-795-4510
Fax: +44(0)151-795-4431
Email: cossina@ilv.ac.uk
Vector has been trimmed from this EST.
Vector has been trimmed from this EST.
Plate: 21 row: c column: 04
Seq primer: pflc T7 (5'-AATACGACTATAGGG-3')
High quality sequence stop: 890.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                          /organism="Spermophilus lateralis"
Mol_type="mRMN"
/db xref="taxon:76772"
/clone="21c04"
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Pred. No. 28;
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AL872732.2 GI:38666145
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Best Local Similarity 52.9%;
Matches 72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr
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(bases 1 to 890)
Williams, D.R., Gracey, A.Y., Martin, S.L., Hughes, M.A., Li, W., Mogers, J. and Cossins, A.R.
Microarray analysis of transcriptional changes during hibernation in the golden mantled ground squirrel, Spermophilus lateralis
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Genome Res. 10 (7), 939-949 (2000)
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SILEO4c2lcO4f1 squirrel embryo library 1 Spermophilus lateralis
CDNA clone 2lcO4 5', mRNA sequence.
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                           Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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     Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
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Spermophilus lateralis
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/organism="Tetraodon nigroviridis"

/mol_type="genomic DNA"

/clone="045G18"

/clone="11b="A"

/clone="10e-"Genoscope sequence ID : COAA045BD09C1

end : T?"
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Laboratory for Environmental Gene Regulation
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/tissue_type="adenocarcinoma"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_39"
/clone_lib="NIH_MGC_39"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: gGGAGAG(0). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies).
                                                                                                                                                                                                                                                                                                                                                                                                                  BE615183 1508 bp mRNA linear EST 24-AUG-2000
601281124F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3623261 5',
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                                                                                                                                                                                 Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tisaue Procurement: ArCc
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomica, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLCM299 row: o column: 06
High quality sequence stop: 307.
                                                                                                                                                                                                                                           134 GTATAATTCCCGTCGTGTGTGGTGACGCCTCACGACGTATTTGTCCGCTGTGCAGAGCG 192
                                                                                                                                                                                                                                                                                           658 cagicacciccacitctaaagccgaggciitragacairitaicinigcigiagagag 716
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases Homo.

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Best Local Similarity 56.4%; Pred. No. 41;
Matches 62; Conservative 0; Mismatches 48;
                                                     DB 5;
                              12.8%; Scor.
54.6%; Pred. No. 30,
... 0; Mismatches

    .1508
    /organism="Homo sapiens"

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/db xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens (human)
                                                                                                  65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nRNA sequence.
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                                                                      Best Local Similarity
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BE615183
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//olone_lib="NGI_CGAP_Mam2"
//note="Organ: mammary; Vector: pCWV-SPORT6; Site 1: Sall;
Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 TGACGTCCCTTCTGGCTCATCCACAAAAACCGTCTCGGGTGGGGTGAGGAGTCCTGGCTGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.mih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agancourt Biosocience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14034 row: a column: 23
High quality sequence stop: 624.
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1 (bases 1 to 945)
MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                           /dev_stages"egg"
/lab.host="Bacherichia coli XLI-blue"
/lab.host="Bacherichia coli XLI-blue"
/clone llb="XGC-egg"
/notes"Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDwas oligo dT primed From 5ug of poly A+ RNA from egg.
EcoRI-NotI cut chonA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end"
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/tiseuc type="tumor, biopsy sample"
/dev stage="5 months"
/lab_nost="DH108"
Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli XL1-blue.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33;
                                                                                                organism="Xenopus tropicalis"
                                                                                                                                                                                                                                                                                                                                                                                                                       12.8%; Score 33.2; D 61.6%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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/strain="FVB/N-3"
/db_xref="taxon:10090"
                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TEggl35n13"
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BQ919900.1 GI:22334586
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Matches 53; Conservative
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                                                                                                                                    BG687472 101-MAY-2001 1054 bp mRNA linear EST 01-MAY-2001 602639444F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4762427 5',
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Plate: LLCM1616 row: h column: 12
High quality sequence stop: 336.
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1 (bases 1 to 1054)

NHH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                     BG687472
BG687472.1 GI:13918869
                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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                                                                                                                                                                                                        mRNA sequence.
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Best Local Similarity
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ORGANISM
                                                                                                    BG687472/c
                                                                                                                                        LOCUS
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EST 22-SEP-2004

linear

mRNA

886 bp

CV242705

RESULT 10 CV242705 LOCUS

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/ Jacks. Track.
/ Jacks. Track.
/ Jab hoste="E. coli DH10B T1 phage resistant cells"
/ clone_lib="PT-MB-N-A-15"
/ clone_lib="PT-MB-N-A-15"
/ note="Vector: pBluescript II SK (+) XR; Site 1: ECORI (5')
end of cDNA); Site_2: XhoI (3') end of cDNA); Terminal
vegetative buds from 20 year old trees harvested near
Corvallis, Oregon on September 19th, 2001. CDNA was
prepared from 5 micrograms of mRNA and directionally
ligated into the pBluescript II SK (+) XR vector using the
pBluescript II XR cDNA Library Construction Kit according
to manufacturer's instructions with modifications
(Stratagene) Plasmid DNA was then transformed by
propagation into DH10B cells (Invitrogen) for
propagation. Normalization was applied according to
published methods (Bonaldo M.F. et al. (1996) Genome
Research 6(9):791 in order to reduce the abundance of
highly expressed transcripts."
                                                                                                                                                                                                                                                                                                                                                                       Ralph.S., Cooper.D., Kolosova,N., Oddy.C., Butterfield,Y.,
Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G.,
Babakaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A.,
Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A.,
Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The poplar transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Joest Bohlmann
Genome BC forest genomics program
University of British Columbia
Micheel Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 123
Tel: 1-604-822-0282
                                                                                                                                                                                                  Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
WS02515.B21_M24 PT-MB-N-A-15 Populus trichocarpa cDNA clone
WS02515_M24_3', mRNA sequence.
CV242705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Populus trichocarpa"
/mol_type="mRNA"
/cultivar="Wild clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: bohlmann@mel.ubc.ca
Plate: W802515 row: M column:
High quality sequence stop: 886.
Location/Qualifiers
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/clone="WS02515_M24"
                                                                                                                                 CV242705.1 GI:52495680
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                                                                                                                                                                                                                                  Populus trichocarpa
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                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murines; Mus:

2 (luosapathi; Muroidea; Murines; Mus:

3 (arninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira; S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funawa, M., Rawai, J., Kduchi, N., Kojima, Y., Matsuyama, T., Itoh, M., Izawa, M., Kawai, J., Kduchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Sugahara, Y., Sato, K., Sahoara, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Yateno, M., Tomaru, Y., Sogaha, Y., Shika, M., Yamamura, T., Yokota, T., Yokota, T., Yokhin, Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

Unpublished (1999)

Contact: Chie Owa
Genome Science Laboratory
                                    AV072177 Mus musculus stomach C57BL/6J adult Mus musculus cDNA clone 2200002K22, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 81-298-36-9145
Fax: 81-298-36-9145
Fax: 81-298-36-9198
Email: genome-researtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S. A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="stomach"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
12.5%; Score 32.6; DB 1; Length 287;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 80; Conservative 0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 AGTCAGTATAATTCCCGTCGTGTGTGTGACGCCTCACGA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 TAIGGITAIGACICCCITITIGGAAGGCIGGGICCIGAAGA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
                                                                                                                                                                            Mus musculus (house mouse)
Mus musculus
                                                                                                                                AV072177.1 GI:5192005
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RESULT 11
AV072177/c
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BP744242
                                                                                                            ACCESSION
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BP744242 Lingulodinium polyedrum cDNA Lingulodinium polyedrum cDNA clone LP13EST52H08, mRNA sequence.

LOCUS DEFINITION

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In (Dases 1 to 251)

El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C., Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J., Fraser,C. and Adams,M.

Donelson,J., Fraser,C. and Adams,M.

Determination of Clone end sequences from Trypanosoma brucei GUTat

10.1 sheared DNA library

Unpublished (1999)

Other GSss: Sheared DNA-21P13.TR

Contact: Najib M. El-Sayed

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ657755 Sheared DNA-21P13.TF Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-21P13, genomic survey sequence.
                                                                                                         Lingulodinium polyedrum

Eukaryota; Alveolata; Dinophyceae; Gonyaulacales; Lingulodinium.

1 (bases 1 to 539)

Tanikawa, N. Akimoto, H., Ogoh, K., Chun, W. and Ohmiya, Y.

Expressed sequence tag analysis of the dinoflagellate Lingulodinium polyedrum during dark phase

Photochem. Photobiol. 80, 31-35 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 CGGGGGGGGGGGGGGGGGGGGGGGGCCCCCCACTGTTGTTCCCAATGACGGCC 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Juleacycderigr.org

Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared

Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared

Clones are derived from the TIGR. Clones will be available for

distribution through ATCC. Sheared DNA end sequences search page:

http://www.tigr.org/tdb/mdb/tbdb/.

Seq primer: M13-Forward

Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
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Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .539
/organism="Lingulodinium polyedrum"
/mol_type="mRNA"
/mol_type="mRNA"
/clone="LP13EST52H08"
/clone_llb="Lingulodinium polyedrum cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Midorioka, Ikeda, OBaka 563-8577, JAPAN
Tel: 81-72-751-7997
Fax: 81-72-751-9628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32.6; DB; Pred. No. 52; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: y-ohmiya@aist.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     15339226
Contact: Yoshihiro Ohmiya
BP744242
BP744242.1 GI:53886462
                                                                                 Lingulodinium polyedrum
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Best Local Similarity 66.2%;
Matches 47; Conservative 0
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E. Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
BAC end sequences of Library PTB
Lupublished
2 (bases 1 to 1527)
2 (bases 1 to 1527)
3 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
L. Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Sciences Center (GSC);
Tel:81-85-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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Pan troglodytes DNA, clone: PTB-126D09.R, genomic survey sequence.
AG118154
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pan troglodytes
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                            /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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Best Local Similarity 50.8%; Pred. No. 61;
Matches 62; Conservative 0; Mismatches
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Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Bubmitted (102-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mall:chimpbes@gc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170,
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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Pan troglodytes DNA, clone: PTB-054E17.R, genomic survey sequence.
AG065034
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                            organism="Trypanosoma brucei".
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Query Match
Best Local Similarity 74.5%; Pred. No. 64;
Matches 41; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Search completed: December 7, 2005, 22:24:30 Job time: 2440 secs

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